

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 109507

TO: Karen A Lacourciere Location: CM1/11D0911E12

Art Unit: 1635

Wednesday, December 03, 2003

Case Serial Number: 08765244

From: Barb O'Bryen

Location: Biotech-Chem Library

CM1-6A05

Phone: 308-4291

BOB

barbara.obryen@uspto.gov

Search Notes

RUSH



STIC-Biotech/ChemLib

From: Sent: To: Cc: Subject:	Fredman, Jeffrey Tuesday, December 02, 2003 2:40 PM STIC-Biotech/ChemLib Lacourciere, Karen FW: Rush sequence search request 08/765,244	
PLEASE RUSH	-1 .	
I Approve.	25/	
Jeff Fredman	CREE	
Original Mess From: Sent: To: Subject:	age Lacourciere, Karen Tuesday, December 02, 2003 2:08 PM Fredman, Jeffrey Rush sequence search request 08/765,244	
Hi Jeff- Could you appi biweek and I di Thanks- Karen	rove a RUSH for this search? It is a short amino acid sequence. The case is a 2 month amended due thi id not realize it had claims to a particular sequence.	is
Please search Thank-you!	SEQ ID NO:22 in the commercial databases and pre-grant publications.	
Karen A. Lacou CM1 11D09 G (703) 308-752 mailbox 11E12	AU 1635	
Searcher: Phone: Location: Date Picked Up: Date Completed: Searcher Prep/Revi Clerical: Online time:	NA Sequences: STN: AA Sequences: DIALOG: Structures: Questel/Orbit: Bibliographic: DRLink: lew: Litigation: Lexis/Nexis: Full text: Sequence Sys.:	

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RESULT 1
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(without alignments)
166.469 Million cell updates/sec
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1: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Mitochondrial matr		nzvm	Drosophila melanog	Drosophila melanod	Mycobacterium spec	Novel human diagno	Drosophila melanog	Neisseria meningit	Bacillus thuringie	Neisseria meningit	Drosophila melanod	S. roseosporus dan	Candida albicans e	Human protein secu		hydroger	Propionibacterium	E.coli cell divisi	A. niger tripentid	Human brain expres	Peptide #11570 enc	Human peptide enco	Protein involved i	Enterococcus faeca	Enterococcus faeca		Protein encoded by	Rianodin receptor,	MH mutant porcine	Ryanodine receptor	Novel human diagno	Human ryanodine re	Peptide MS-34, wit	Human transferrin	Human secreted pro
AAB15704	AAB22835	AAU23468	ABB57741	ABB59259	AAY04933	ABG29304	ABB59241	AAY75465	AAR96126	AAY75466	ABB64170	ABP62760	ABP73265	AAB93938	AAB94042	AA018173	AAU60044	AAR78184	ABR38858	AAM64583	AAM37533	ABG46393	AAY37084	AAU33373	AAU35205	AAG89868	AAB07559	AAR10834	AAR25450	AAR11510	ABG04969	ABB11480	AAY57007	ABB10986	AAG03218
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31	31	149	866	755	165	774	1124	138	1169	138	296	2379	564	746	975	975	74	457	624	75	75	75	185	285	334	684	688	4987	5035	5072	5081	9	13	93	96
36.6	36.6	26.0	24.9	24.7	24.0	24.0	24.0	23.7	23.5	23.3	23.3	23.3	23.0	23.0	23.0	23.0	22.6	22.6	22.6	22.4	22.4	22.4	22.4	22.4	22.4	22.4	22.4	22.4	22.4	22.4	22.4	22.4	'n	22.1	'n
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10	11	12	13				17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 5

ALIGNMENTS

promoter; peptide-nucleic acid; cyclised; gene therapy; target; site-directed mutagenesis; introduction; protein transport. Rat ornithine transcarbamylase signal peptide. AAR90584 standard; Protein; 43 AA. 95DE-1020815. 94DE-4421079. (updated)
(first entry) WPI; 1996-041226/05. Seibel A, Seibel P; (SEIB/) SEIBEL P. DE19520815-A1 16-JUN-1994; 11-JUN-1995; 25-MAR-2003 31-OCT-1996 21-DEC-1995; Synthetic. AAR90584;

Replicable and transcriptionally active plasmid carrying signal peptide for specific target - useful for site directed mutagenesis

us-08-765-244-22.rag

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(TANA/) TANAKA M.
(GIFU-) ZH GIFUKEN KOKUSAI BIO KENYUJO.
(OYOS-) ZH OYO SEIKAGAKU KENKYUSHO.
                                                                                                                                                                                                             14-DEC-2000; 2000JP-0380975.
                                                                                                                                                                                                                     14-DEC-2000; 2000JP-0380975
                                                                                                                                                                                                                                         WPI; 2002-569946/61
                                                                                                                                                                                               JP2002176988-A.
                                                                                                                                                               07-OCT-2002
                                                                                                                                                                              Rat; signal recombinant
                                                                                                                                                                                                      25-JUN-2002
                                                                                                    Sequence
                                                                                                                                                        ABG30857;
                                                                                                          Query Match
                                                                                                                 Matches
                                                                                                                                             RESULT 2
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Two modified oligonuclectides (introducing PstI and XhoI sites) were used to amplify a region of the human mitochondrial (mt) genome contg. the light strand promoter, mtDNA ori of the heavy strand, CSB's ("conserved sequence blocks") and a regulation site for DNA replication. Behind this fragment (5' direction) a synthetic multiple cloning site was introduced, generating a product with overhanign ends. The synthetic region also introduced a bidirection) a synthetic fragment and pBluescript sequence. The amplification product, synthetic fragment and pBluescript were ligated and recombinant plasmid 1 (AAT12315) was produced. Human mt incleotide) was isolated by PCR from chloramphenicol resistant Hela colls and inserted into plasmid 1 to form plasmid 2 (AAT12316). The colls and inserted into plasmid to form plasmid 2 (AAT12316). The colls and insert was isolated as a BsaI fragment and cyclised using hairpin clopo oligonucleotides, one of which carried the required signal peptide the present sequence. The wolfication, the signal peptide was attached after cyclisation. The new plasmids were able to impart chloramphenicol resistance to otherwise sensitive B lymphocytes and fibroblasts. Similar plasmids without a signal peptide could not do this. The material parametric collection when the signal peptide could not do this. The material collection with an angelial peptide could not do this. The material collection whence the cells, so fire directed materials and product whence the collection with a signal peptide could not do this. The material collection whence the collection with the collection whence the c
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and molecular therapy of genetic diseases
                                                                                                                                                                                  Disclosure; Column 11; 24pp; German.
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.; 0 Match 100.0%; Score 217; DB 17; Length 43; Local Similarity 100.0%; Pred. No. 3.1e-26; les 43; Conservative 0; Mismatches 0; Indels Indels 1 MLSNIRILLNKAALRKAHTSMVRNFRYGKPVOSQVQLKPRDLC 43 1 MLSNLRILINKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDLC 43 43 AA;

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Gaps

ABG30857 standard; Peptide; 32 AA (first entry)

Rat ornithine transcarbamylase signal peptide.

peptide; ornithine transcarbamylase; vector; fusion protein; extranuclear

N-PSDB; ABK88419

A recombinant vector for expressing a fused protein, useful for decomposing an extranuclear gene of a nonhuman organism -

Disclosure; Page 3; 15pp; Japanese.

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               The invention relates to a recombinant vector for expressing a fused protein containing a fused gene in which a base sequence defining a transfer signal peptide to small cellular organs having an extranuclear gene is combined with a base sequence defining the amino acid sequence
                                                                                         a restriction enzyme recognising a defined base sequence. The vector is used for decomposing an extranuclear gene of a nonhuman organism. The present sequence represents the signal peptide of rat mitochondrial ornithine transcarbamylase (MOT) which may be used in the vector of the
                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                    Length 32;
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Pred. No. 2.4e-17;
0; Mismatches 0;
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100.0%; Pre
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Best Local Similarity
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hypotonia; autism; sudden infant death syndrome; hypoglycemia; leukaemia; thrombocytopenia; migraine; hearing loss; stroke; troke; refractory; infantile reflux; carnitine deficiency; multiple sclerosis; blindness; optic atrophy; renal tubular acidosis; cardiomyopathy; chronic pancreatitis; ATPase 6. Leber hereditary optic neuropathy; myoclonic epilepsy; neurogenic muscular weakness; ataxia; retinitis pigmentosa; Kearns-Sayre syndrome; Leigh syndrome; Pearson Marrow pancreas syndrome; aminoglycoside-associated deafness; diabetes; deafness; leukodystrophy; Mitochondrial genome; mitochondrial encephalmyopathy; lactic acidosis; Protein encoded by plasmid pUOATP2. (first entry) 15-JAN-2001

AAB18445 standard; Protein; 258 AA

RESULT 3

Synthetic.

WO200053773-A2

08-MAR-2000; 2000WO-US06037,

08-MAR-1999;

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Zullo SJ,

2000-565602/52. WPI; 2000-565602/ N-PSDB; AAA75084.

or deletions Functionally complementing one or more defects, mutations, or delet in a mitochondrial genome of a cell, useful for treating diabetes w deafness, comprises introducing mitochondrial DNA into the nuclear denome -

Example 1; Fig 3; 49pp; English.

one or more defects, mutations, or deletions in a mitochondrial genome of a cell having a nuclear genome. The method is used for treating a disease or disorder that arises from deletion of the protenn-encoding genes of the mitochondrial genome. Alternatively, the method is used for treating a disease or disorder that arises from one or more defects, deletions or The specification describes a method for functionally complementing

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Transcription and translation in the mitochondria. The diseases or disorders that can be ameliorated are mitochondria. The diseases or disorders that can be ameliorated are mitochondrial encephalmyopathy with lactic acidosis and stroke-like episodes, Leber hereditary optic muscular weakness, ataxia, retinitis pigmentosa, Kaarns-Sayre syndrome, muscular weakness, ataxia, retinitis pigmentosa, Kaarns-Sayre syndrome, santoplacomid-sayre syndrome, mitorated deafness, diabetes with deafness, leukodystrophy with hypotonia, autism with seizures, sudden infant death syndrome with hypotonia, autism with seizures, sudden infant death syndrome with hypotonia, autism with seizures, sudden infant death syndrome with hypotonia, leaved with hearing loss, strokes, or diabetes), early maring loss, refractory infantile reflux with carnitine deficiency, multiple sclerosis with seizures, blindness with optic atrophy and dystomia, renal tubular acidosis with elevated lactic acid and hypotonia, nonvalvular hypertrophic cardiomyopathy before age 50 and chronic pancreatitis with stroke-like episodes. The present sequence is encoded by plasmid puoArPP2 comprises a mucant oligomycin-cesistant ATPase 6 mitochondrial gene derived from Chinese hamster ovary (CHO) cells linked to ornithine transcarbamylase DNA sequence. It is used for targeting the protein to the mitochondria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a recombinant vector for expressing a fused protein containing a fused gene in which a base sequence defining a transfer signal peptide to small cellular organs having an extranuclear gene is combined with a base sequence defining the amino acid sequence of a restriction enzyme recognising a defined base sequence. The vector is used for decomposing an extranuclear gene of a nonhuman organism.
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  mutations in mitochondrial genes encoding ribosomes or tRNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 109, DB 21; Length 258;
Pred. No. 2e-08;
2; Mismatches 12; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; signal peptide; ornithine transcarbamylase; MOT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant vector; fusion protein; extranuclear gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLFNLRILLINNAAFRNGHNFWVRNFRCGOPLOMNENL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ornithine transcarbamylase signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GIFU-) ZH GIFUKEN KOKUSAI BIO KENYUJO.
(OYOS-) ZH OYO SEIKAGAKU KENKYUSHO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG30856 standard; Peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.2%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 AA;
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The present sequence represents the signal peptide of human mitochondrial ornithine transcarbamylase (MOT) which may be used in the vector of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method for preparing a protein which interacts with the heat shock protein HSP47. The method involves the two-hybrid screening method using the HSP47 gene and a mammalian cDNA library. The HSP47 interacting proteins are useful for the diagnosis and treatment of diseases caused by an increase or decrease in activity of HSP47. The present sequence was used in an example from the present
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                                                                                   49.8%; Score 108; DB 23; Length 32; 68.8%; Pred. No. 2.2e-09; ive 2; Mismatches 8; Indels
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                                                                                                                                             1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQ 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 12; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR48260 standard; peptide; 32 AA.
                                                                                                                                                                                                                                                AAG64224 standard; Peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0330631.
                                                                                                                                                                                                                                                                                                      19-SEP-2001 (first entry)
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(first entry)
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hes 22; Conservative
                                                                                                                                                                                                                                                                                                                                   OTC peptide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
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29-JUL-1994
                               invention.
                                                                                                                                                                                                                                                                           AAG64224;
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Matches
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AAR48260
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endoplasmic reticulum.

Mitochondrial matrix retention signal,

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New vector systems comprise a sequence adapted for intracellular delivery and expression contg. a promoter operably linked to an antibody gene encoding an antibody which binds to a specific target antigen. The antibody is esp. a single chain antibody in which the heavy and light chain variable regions are joined via a hydrophilic linker peptide. Localisation sequences are pref. included in the constructs. The sequence AAR48260 is a mitochondrial matrix retention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Intracellular binding of antigens - by using antibody targetting with vector system, for e.g. tumour suppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody; immune response; modulation; MHC; IRM; receptor; intrabody; major histocompatibility complex; graft rejection; immunomodulatory response molecule; regulation; transplantation; retention signal; localisation signal; golgi apparatus; ER;
                                                                                           Single chain antibody; sFv; heavy chain; light chain; variable domain; hydrophilic linker; antibodies; targetting; subcellular localisation signal; mitochondrial matrix; retention signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.4%; Score 92; DB 15; Length 32; 61.3%; Pred. No. 6.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "not defined"
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                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Intracellular binding to a desired target by an intracellularly expressed antibody (i.e. an intrabody) can be used to knock out multiple locuses of immunomodulatory receptor molecules (IRMs), so that the expression of multiple major histocompatibility (MHC) molecules is blocked. This selective targeting of IRMs, their pathways or components, can be used to selectively regulate the immune system by controlling expression of these molecules and preventing an undesired immune response in a cell. Any component of the MHC pathway or the MHC assembly line or antigen presentation of the Engaged. Intrabodies can be used to knock out the immune response in a particular tissue or portion of the body to prepare it for cell or tissue transplantation. Alternatively, an organ for intrabodies can comprise whole antibodies, heavy chains, Fab' intrabodies an intracellular localisation signal to facilitate interception of expressed proteins. For example, if the target was interception of expressed proteins. For example, if the target was an interception of expressed proteins. For example, if the target was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a cell surface receptor, the antibody would comprise a leader sequence and an endoplasmic reticulum (ER) or Golgi apparatus retention signal. This peptide is a localisation sequence for the mitochondrial matrix. For other localisation sequences see
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61.3%; Pred. No. 6.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                              Altering the regulation of the immune system
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                                                                                                                                  amino acid"
                                                                                                 'note= "Any amino acid"
                                                                                                                                                                  /note= "Any amino acid"
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                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 28; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG92993 standard; Peptide; 32
                                                                                                                                  "Any
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                                                                                                                                                                                                                                                                                                                                                             Marasco W, Mhashikar A;
                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-229546/19.
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                                                                 Key
Misc-difference
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                                Synthetic
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10; Indels

The invention discloses a method for identifying polymuclectides encoding a regulator polypeptide, whose expression induces activation of a target transcriptional regulatory region in a host cell. The method comprises providing a population of eukaryotic host cells capable of expressing the polypeptides, introducing into the host cells a library of polymucleotides and then polypeptides, permitting expression of the polypeptides and then recovering them from the host cells. The target transcriptional equal product, the expression of which results in host cells dath or cause the host cells to exhibit a pre-determined modified phenotype and where the host cells to exhibit a pre-determined modified phenotype and where the host cells to exhibit a pre-determined modified phenotype and where the product is expressed upon activation of target transcriptional regulatory region. Each candidate regulator polypeptide comprises a candidate peptide and a molecular scaffold fused to the peptide so that the peptide is displayed on the surface of the candidate regulator polypeptide and a molecular scaffold fused to the peptide so that the peptide is displayed on the surface of the candidate regulator properties. The methods are useful in selecting and/or screening regulator molecules, such as polypeptides, which directly or indirectly induce or suppress the transcriptional activation of a target transcriptional regulator, region in a enkaryotic host cell. These regulator molecules may be used (e.g. in gene therapy) for preventing or treating cancers (e.g. breast or ovarian cancer), cardiovascular diseases (e.g. psoriasis), infections (e.g. viral, bacterial), acquired inmunodeficiency syndrome (AIDS), in cosmetic applications and in wound healing. The method is also useful in screening regulator molecules and din improving the performent and drug cancers allergic response and in hiptoreducing the performent of persented in ABG92946-ABG93029 are examples of regulator polypeptides. transcriptional regulatory regions, useful for treating cancer, comprises introducing host cells expressing the polypeptide into a Identifying regulator polypeptides which influence target Disclosure, Page 37; 224pp; English. 05-FEB-2001; 2001US-265880P. 27-FEB-2001; 2001US-271423P. 23-JAN-2001; 2001US-26226P. 28-MAR-2000; 2000US-122586P. 04-FEB-2002; 2002WO-US02814, 2001US-265589P. 97US-935377P library of polynucleotides (UYRP) UNIV ROCHESTER. WPI; 2002-643398/69. WO200262822-A2. Unidentified. 02-FEB-2001; 22-SEP-1997; 15-AUG-2002. Zauderer M,

Gaps ò 42.4%; Score 92; DB 23; Length 32; llarity 61.3%; Pred. No. 68-07; Conservative 2; Mismatches 10; Indels Best Local Similarity Matches 19; Conserv Sequence Query Match

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Identification; intrabody; eukaryotic cell; immunoglobulin; selection; cardiovascular; diminished arrhythmia potential; cardiomyocyte; stroke; enhanced contractile property; heart failure; arrhythmia; embolic; sarcolemmal calcium cycling; artery, arteriole; angina; atherosclerosis; LDL metabolism; HDL metabolism; skin biology; keloid formation.
                                                                                                                                                               Mitochondrial matrix targeting peptide SEQ ID NO:54.
  1 MLSNLRILLINKAALRKAHTSMVRNFRYGKPV 31
                       1 MLFNLRXXLNNAAFRHGHNFMVRNFRCGOPL 31
                                                                                       ABP56588 standard; Peptide; 32 AA.
                                                                                                                                      (first entry)
                                                                                                                                      24-MAR-2003
                                                                                                                ABP56588;
                                                                           ABP56588
                                                                                                 Regulator; transcription; cell death; phenotype; molecular scaffold; gene therapy; cardors cardiovascular disease; arrhythmis; heart failure; ischaemia; obesity; neurodegenerative disease; Alzheimer's disease; bone pathology; dermatologic disease; psoriasis; infection; AIDS; acquired immunodeficiency syndrome; cosmetic; wound healing; antibiotic transport; drug toxxicity; drug resistance; immunobiology; inflammation; allergic response; human immunodeficiency virus.
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(UYRP) UNIV ROCHESTER MEDICAL CENT. 23-JAN-2001; 2001US-263225P. 24-JAN-2001; 2001US-263200P. 27-FEB-2001; 2001US-271422P. 15-JUN-2001; 2001US-298095P. 23-JAN-2002; 2002WO-US01677. Wei C, WO200286096-A2. 31-OCT-2002. Zauderer M,

'note= "any amino acid" /note= "any amino acid" /note= "any amino acid"

Location/Qualifiers

Misc-difference 7 Misc-difference 8 Misc-difference

Unidentified.

Selecting polynucleotides encoding an intracellular immunoglobulin which induces a modified phenotype in a eukaryotic host cell, by introducing library of polynucleotides encoding immunoglobulin subunit WPI; 2003-103408/09.

Disclosure; Page 44; 257pp; English.

polypeptides

The present invention describes a method for selecting polynucleotides (PNS) encoding an intracellular immunoglobulin molecule or its fragment whose expression induces a modified phenotype in a eukaryotic host cell (I). The method comprises introducing into (I) a first and second library of PNS encoding, through operable association with a transcriptional control region, first and second intracellular immunoglobulin subunit polympetides, respectively. The method is useful for selecting polymucleotides which encode an intracellular immunoglobulin molecule, or fragment. The method as useful e.g. for identifying polymucleotides which sensitise host cells to killing by an agent. The method may also be used in cardiovascular applications, for screening for diminished arrhythmia potential in cardiomycoytes and for enhanced contractile arrhythmia potential in cardiomycoytes and diminish heart failure potential; for identifying intracellular immunoglobulin molecules that will regulate intracellular and sarcolemmal calcium cycling in cardiomycoytes to prevent arrhythmias or that will diminish embolic phenomena in arteries

therapy for the treatment of disorders such as Alzheimer's disease.

ij

Gaps

1;

Length 31; Indels

Score 79.5; DB 21; Pred. No. 5.8e-05; 1; Mismatches 10;

36.6%;

Local Similarity

Query Match Matches

31 AA;

Sequence

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in atherosclerosis-producing mechanisms to find intracellular immunoglobulin molecules that regulate LDL and HDL metabolism; in skin biology applications; and in regulating or inhibiting keloid formation. ABZ22379 to ABZ22449 and ABF56536 to ABP56618 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a localisation sequence that can be used to direct stabilised single-chain antibodies to the mitochondrial matrix. The N-terminus of the single-chain antibody is linked to a stabilising fusion peptide, referred to as a stabilon, which increases stability of the antibody against proteolysis in vivo. Degradation of the antibody may be modulated by linking the stabilon to the antibody through a protease-sensitive linker region. The stabilon is removed upon induction of expression of a specific restriction protease by means of an inducible promoter, and this renders the antibody susceptible to proteolysis by the N-end rule pathway. This method for regulating protein stability allows removal of the antibody after it has bound to its target antigen. Stabilised recombinant proteins may be used in gene
and arterioles leading to strokes and angina; in screening for decreases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrial matrix localisation sequence; single-chain antibody; stabilon; stabilising fusion peptide; vaccine; gene therapy; protein degradation modulation; protein stability; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating degradability of protein or peptide useful for gene therapy involving antibodies, comprises altering a gene at the N terminus to render protein or peptide metabolically stable -
                                                                                                                                                                                                               Gaps
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                                                                                                                                                                      ch 42.4%; Score 92; DB 24; Length 32; 1 Similarity 61.3%; Pred. No. 6.8e-07; 19; Conservative 2; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrial matrix localisation sequence.
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(MCIN/) MCINNIS P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 50; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                         AAB15704 standard; Peptide; 31
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                                                                                                                                  32 AA;
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                                                                                                                                    Sequence
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Best Local
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The invention relates to a controlled release drug delivery system.

Target cells in a patient are transformed with an expression construct encoding an antibody (particularly a single chain antibody) to the drug to be delivered. The antibody contains a modulator of intracellular half-life; this can either be a stabilising or destabilising residue of ("stabilon") containing a stabilising residue linked to the antibody N-terminus via a protease cleavage site. On administration of the drug, N-terminus via a protease cleavage site. On administration of the drug, the antibody binds the drug, localising it at the target cells but maintaining it in an inactive state. As the antibody is degraded (the mainescale for which is dependent upon the N-terminal or stabilon amino acids), the drug is released at its site of action where it can exert its effects. The antibody encoded by the expression construct (and clids), the therapeutic agent) can be targetted to particular subcellular localisation signals. The novel method may be used to deliver therapeutic agents to patients with a variety of conditions such as
                                                                                                                                                                                  Controlled release delivery system; drug targetting; drug-specific antibody; intracellular half-life; gene therapy; diabetes; autoimmune disease; inflammatory disease; infectious disease; cancer; side effect; subcellular localisation sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Delivering a drug, to a patient suffering from cancer or diabetes, at a predetermined site, comprises altering a target cell to express a drug specific antibody by gene therapy and administering the drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.
                                                                                                                                               Mitochondrial matrix localisation signal.
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                         /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                              /label= unknown
                                 AAB22835 standard; peptide; 31
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                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                Unidentified
                                                                                                           10-JAN-2001
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                                                                      AAB22835;
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RESULT 11
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2000US-0226681.
2000US-0226868.
2000US-0227182.
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2000US-0231242.
2000US-0231243.
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000US-0233063
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2000US-0241787
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26-SEP-20
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               diseases and especially cancer. The delivery method of the invention causes a drug to become almost immediately localised at its site of action in an inactive form where it accumulates. Once released by antibody degradation, the drug is at an effective concentration only at the target site, with very little free drug being available in the rest of the body. The system of the invention therefore reduces the side effects caused by therapeutic agents, and also provides economic benefits as a smaller amount can be administered to the patient. Sequences AAB22835 and ABB22837 represent subcellular localisation the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cardiovascular disorder; anti arthritic; nephrotropic; anticoagulant.
                                                                                                                                                                                                                                                                                                                         Gaps
           infectious
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                                                                                                                                                                                                                                                                                   Length 31;
                                                                                                                                                                                                                                                                                                                       Indels
diabetes, autoimmune diseases, inflammatory diseases,
                                                                                                                                                                                                                                                                                 36.6%; Score 79.5; DB 21; 61.3%; Pred. No. 5.8e-05;
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                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human enzyme polypeptide #554.
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04-FEB-2000; 2000US-0180628.

02-MAR-2000; 2000US-018664.

16-MAR-2000; 2000US-018974.

17-MAR-2000; 2000US-0189123.

19-MAY-2000; 2000US-0189123.

19-MAY-2000; 2000US-0209467.

28-JUN-2000; 2000US-0215135.

07-JUN-2000; 2000US-0216486.

07-JUL-2000; 2000US-0216487.

11-JUL-2000; 2000US-021647.

07-JUL-2000; 2000US-0216487.
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2000US-0220963
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nes 19; Conservative
                                                                                                                                                                                                                                             31 AA;
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AA023468
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Length 149;

22;

26.0%; Score 56.5; D 35.3%; Pred. No. 1.6; ive 7; Mismatches

40 15;

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                         N-PSDB; AAS41338
                                                                                     17-NOV-2000;
17-NOV-2000;
                                                                                                                                               08-DEC-2000;
                                                     17-NOV-2000;
                                                               7-NOV-2000;
                                                                   17-NOV-2000;
17-NOV-2000;
                                                                                                  L7-NOV-2000;
                                                                                                                    01-DEC-2000;
                                                          7-NOV-2000;
                                                                                              17-NOV-2000;
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                                                                                                           17-NOV-2000;
                                                                                                                                                                                                                                                                                                                     nvention.
                                                                                                                                                                                           Rosen CA,
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher evkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                          LRMTLOKESAMIARSRKPHATMIRNAKYSGLHAGWSLWLPVESALOSHOPR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 15; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 15.
                                                                                                                                                                                5 LRILLINK-----AALRKAHTSMVRNFRYG--
                                                                                                                                                                                                                                                                                                                                       ABB57741 standard; Protein; 866 AA
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11-JUL-2000; 2000US-0614150.
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Matches 15; Conservative
                                                                                                         Best Local Similarity 35.3
Matches 18; Conservative
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N-PSDB; ABL01844.
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                                               149 AA;
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ANUZ2915-AAUZ2814 represent the novel human enzyme polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
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08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246528.
08-NOV-2000; 2000US-0246532.
08-NOV-2000; 2000US-0246619.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246611.
17-NOV-2000; 2000US-0246613.
17-NOV-2000; 2000US-0249207.
17-NOV-2000; 2000US-0249209.
17-NOV-2000; 2000US-0249209.
17-NOV-2000; 2000US-0249209.
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2000US-0249297.
2000US-024929.
2000US-0249300.
2000US-0250301.
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2000US-0249216.
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2000US-0249245.
2000US-0249264.
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2000US-0249213
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2000US-0251856
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2000US-0251990
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Myers EW;

PWD,

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Gaps

12;

7; Indels

24.9%; Score 54; DB 22; 33.3%; Pred. No. 33; ive 11; Mismatches 7,

41

RESULT 14

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Length 866;

Goguet de la Salmoniere Y;

Portnoi D,

Pelicic V,

98WO-FR01813, 97FR-0011325. 97FR-0010404.

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proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
                                                                                                                                                                                                                                                                                                                                            Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted
                                                                                                                                                                                                                                                        Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 RILLNKAALRKAHTSMVRNFRYGKPVOSQVQLKPR
                                                                                                                                                                                                                                                                                                                   Claim 32; Fig 38B; 309pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 24.0%;
|| Similarity 37.1%;
| 13; Conservative
                                                                                                                                              (INSP ) INST PASTEUR
                                                                                                                                                                          Lim EM,
                                                                                                                                                                                                                  WPI; 1999-181045/15.
N-PSDB; AAX34186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                165 AA;
                   WO9909186-A2
                                                                         14-AUG-1998;
                                                                                                       11-SEP-1997;
                                                                                                                    14-AUG-1997;
                                                                                                                                                                       Gicquel B,
Guigueno A;
                                               25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Matches
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Job time
    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ARBENTATABUTZOTZ).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 4569; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 755;
                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 4569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53.5; DB
Pred. No. 33;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Myers EW;
                ABB59259 standard; Protein; 755 AA.
                                                                                                                                                                                                                                                                                                                                                         PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.7%;
                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                        ï
                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                    2001-656860/75,
                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABB57737-ABB72072)
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tes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   755 AA;
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860,
N-PSDB; ABL03362
                                                                                                                                                                                                  WO200171042-A2
                                                                                                                                             pharmaceutical
                                                                                                                                                                                                                              27-SEP-2001
                                            ABB59259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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ABB59259
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completed: December 3, 2003, 14:32:33
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<u>ب</u>

Gaps,

<u>ب</u>

Indels

15;

Conservative

Best Loc Matches

||:|| | | ||||| : : ||||| LSDLRRELE--VLRKAHFBELDHLFYGTG-QPEAEAKPRD 47 2 LSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRD 41

Secreted protein, Mycobacterium, primer, PCR; amplification, probe, hybridisation, detection, vaccine, immunisation, infection.

Mycobacterium sp

Mycobacterium species protein sequence 38B.

(first entry)

06-JUL-1999

AAY04933;

AAY04933 standard; Protein; 165 AA

RESULT 1: AAY04933

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Gaps

,; ;

12; 40

Score 52; DB 20; Pred. No. 8.9; 8; Mismatches 12

Length 165; Indels us-08-765-244-22.rai

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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32812,
Sequence 18053,
Sequence 2, Appl
                                                                                                            ; Search time 22 Seconds
(without alignments)
82.698 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                     1 MLSNLRILLINKAALRKAHTS.......NFRYGKPVQSQVQLKPRDLC 43
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Sequence 42
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Sequence 29
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Sequence 5
Sequence 1
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Sequence 1
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Sequence
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/cgm2_6/prodata/1/iaa/5B_COMB.pep:*
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/cgm2_6/prodata/1/iaa/PcTUS_COMB.pep:*
/cgm2_6/prodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-350-215-29
US-09-287-145A-29
US-09-556-111-29
US-09-413-814-42
US-09-252-991A-32812
US-09-252-991A-32812
US-08-542-91A-32812
US-08-542-921-2
US-08-880-685-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-107-532A-5399
US-09-252-991A-18693
US-09-457-708-2
                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-732-210-98
                                                                                                                                                                                                                                                                                                                  328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                        December 3, 2003, 14:31:47
                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                  US-08-765-244-22
217
                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                          Run on:
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Sequence 10, Appl	Sequence 10, Appl	Sequence 15, Appl	Sequence 15, Appl	Sequence 32535, A			Sequence 28901, A			Seguence 5110. Ap	10,	Sequence 20, Appl	Sequence 5, Appli	Sequence 5. Appli	Ä	_	
US-08-582-776C-10	US-08-434-831B-10	US-08-313-553-15	US-08-767-993-15	US-09-252-991A-32535	US-09-914-259-68	US-09-585-858-27	US-09-252-991A-28901	US-09-328-352-4817	US-09-312-762A-14	US-09-107-532A-5110	US-08-671-757A-10	US-09-219-983A-20	US-07-846-181-5	US-07-845-989-5	US-09-252-991A-19085	US-09-328-352-6926	US-09-252-991A-26810
m	m	Н	m	4	4	4	4	4	4	4	4	4	н	ч	4	4	4
1711	1711	559	559	729	1139	761	236	275	532	609	700	716	730	730	795	984	1124
21.4	21.4	21.2	21.2	21.2	21.2	21.0	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.7
46.5	46.5	46	46	46	46	45.5	45	45	45	45	45	45	45	45	45	45	45
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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US-064-73-190-29

WG-064-73-190-29

Requence 29 Application US/08373190

Referent No. 585-182

GENERAL INTROMATION:

APPLICANT: HASELTINE, WILLIAM

TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS

NUMBER OF SEQUENCES: 79

CORRESPONDENCE ADDRESS:

ADDRESSER: 1130 WATER STREET

CITY: BOSTON

STRET: 130 WATER STREET

CITY: BOSTON

STRET: 130 WATER STREET

COMPUTER: MA

COMPUTER: BASELSON VERSION

MEDIUM TYPE: DS

COMPUTER: IBM COMPATION

MEDIUM TYPE: 105/09

COMPUTER: IBM COMPATION

MEDIUM TYPE: 105/09

COMPUTER: 106-701-1993

PILING DATE: 1-JUL-1993

PRILING DATE: 1-JUL-1993

PRILING DATE: 10-JUL-1993

PRILING DATE: 11-JUL-1993

REGISTRATION NUMBER: 34,235

PRILING DATE: 107-23-4400

TELEFAX: 617-523-4400

TELEFAX: 617-523-4400

TELEFAX: 617-523-4400

TELEFAX: 617-523-6440

TELEFAX: 617-6440

TELEFAX: 617-623-6440

TELEFAX:
```

DB 2; Length 32;

42.4%; Score 92;

```
APPLICANT: MARRAGO, WAYNE
APPLICANT: HASELTINE, WILLIAM
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
                                                                                                            ZIP: 02109
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,215
FILING DATE: 12-DEC-1994
CLASSIFICATION '514
ATTORNEY/AGENT INFORMATION:
RAME: BISENSTEIN, RONALD I.
RAME: BISENSTEIN, RONALD I.
RESISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956-CP3
FILECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-6440
TELERAX: (617) 523-6440
TELERAX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
TWANTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/287,145A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.4%; Score 92; DB 3; Best Local Similarity 61.3%; Pred. No. 9.2e-08 Matches 19; Conservative 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/438,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29, Application US/09287145A Patent No. 6072036 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: EISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 4195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
                                           MASSACHUSETTS: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-350-215-29
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                                                                                                         02109
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                                           ö
                                                                                                                                                                                                                                                                                                                                      Sequence 29, Application US/08438190A
Patent No. 5965371
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
APPLICANT: HASELTINE, WILLIAM
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/08350215
Patent No. 6004940
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE A.
APPLICANT: RICHARDSON, JENNIFER
TITLE OF INVENTION: INTRACELLULAR TARGETING OF ENDOGENOUS
TITLE OF INVENTION: POTTEINS
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,190A
   61.3%; Pred. No. 9.2e-08; tive 2; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.4%; Score 92; DB 2;
61.3%; Pred. No. 9.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLFNLRXXINNAAFRHGHNFMVRNFRCGQPL 31
                                                                                                         1 MLSNLRILLINKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                       1 MLFNLRXXLNNAAFRHGHNFMVRNFRCGOPL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATE:
FILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: EISENSTEIN: RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956
TELEPHONE: (617) 523-6440
TELEPAX: (617) 523-6440
TELEFAX: (617) 523-6440
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 WATER STREET
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Best Local Similarity 61.33
Matches 19; Conservative
Best Local Similarity 61.3
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
GY: linear
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TOPOLOGY:
US-08-438-190A-29
                                                                                                                                                                                                                                                                                    RESULT 2
US-08-438-190A-29
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US-08-350-215-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Length 32;

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APPLICANT: Mueller, Joachim
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DATE SEQUENCES OF ENTYMENT PRINTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT PAPLICATION NUMBER: US/09/413,814
EARLIER PILING DATE: 1999-10-07
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 42
                                                 Sequence 42, Application US/09413814

Patent No. 6225064

### Sequence 52, Application US/09413814

#### APPLICANT: Brand: Petra

#### APPLICANT: Brand: Petra

#### APPLICANT: Globerg: Setra

#### APPLICANT: Globerg: Steven L

#### APPLICANT: Globerg: Steven L

#### APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 AALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.9%;
35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 35.5
les 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-252-991A-32812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-32812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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Matches
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ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS
CUSHMAN
                                                                                                                                                                                                      42.4%; Score 92; DB 3; Length 32; 61.3%; Pred. No. 9.2e-08; Live 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.4%; Score 92; DB 4; Length 32; 61.3%; Pred. No. 9.2e-08; ive 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MARASCO, WAYNE
APPLICANT: MARASCO, WAYNE
HASELTINE, WILLIAM
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING
PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/556,111
FILING DATE: 21-Apr-2000
CLASSIFICATION: Unknown>
PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: 08/438,190
FILING DATE: CURROWN>
ATTORNEY/AGBYT INFORMATION:
NAME: EISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956
TELECOMMUNICATION INFORMATION:
TELEBROOME: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                       1 MLFNLRXXLNNAAFRHGHNFMVRNFRCGQPL 31
                                                                                                                                                                                                                                                                                             1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/09556111 Patent No. 6329173 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 32 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
(617) 523-6440
                TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                    Query Match
Best Local Similarity 61.3
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                          US-09-287-145A-29
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-09-556-111-29
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TELEFAX:
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Gaps

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Indels

8; Mismatches

Length 2539;

DB 3;

Score 54; Pred. No.

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LOCATION: (451)
OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
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                                                                                                                     Sequence 32812, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILLS OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILLING DATE: 1399-02-18

PRIOR PELING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
7 ILLNKAALRKAHTSMVRNFRYGKPVQSQVQLK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.4%; Score 53; DB .34.4%; Pred. No. 4.1; tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 34.4%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---KAALRKAHTSMVRNFRYG---KPVQSQVQLKPRDL 42
                                                                                                                                                                                                 23.5%; Score 51; DB 1; Length 1169; 25.5%; Pred. No. 28; tive 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.5%; Score 51; DB 2; Length 1169; 25.5%; Pred. No. 28; 15; Indels ive 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: IIZUKA, TOSHIHIKO
APPLICANT: TAGAWA, MICHITO
APPLICANT: ARAI, SAFOSHI
APPLICANT: ARAI: SAFOSHI
APPLICANT: MIZEKI, MASATSUGU
APPLICANT: MIYAKE, TOSHIRO
TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPOURS: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,685
FILING DATE: 23-UN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/542,921
FILING DATE: 13-OCT-1995
APPLICATION NUMBER: US 08/542,921
FILING DATE: 14-OCT-1994
ATTORNEY-ARENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08880685
Patent No. 5834296
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 413-3000
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENTE: 1169 amit-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                          SEQUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
                                                                                                                                                                                         Query Match
Best Local Similarity 25.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
23.5.
Best Local Similarity 25.5
Matches 14; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-542-921-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-880-685-2
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                                                                           amino acid
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                                                                                                                                                         APPLICANT: MARCO.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRGIGNOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18053

LENGTH: 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 52, DB 4, Length 218;
Pred. No. 2.4;
6, Mismatches 20, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSES: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ARAI, SATOSHI
APPLICANT: NIIZEKI, MASATSUGU
APPLICANT: NIYAKE, TOSHIRO
TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONTWARD: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,921
FILING DATE: 13-OCT-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US/08/542,94
PRIOR APPLICATION NUMBER: US/08/54
APPLICATION NUMBER: US/08/54
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
                                                                                      Sequence 18053, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08542921
Patent No. 5736514
GENERAL INFORMATION:
APPLICANT: IZUKA, TOSHIHIKO
APPLICANT: TAGAWA, MICHITO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-18053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: 2 (703) 413-2220
TELEX: 2 (403) 413-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.0%;
nilarity 33.3%;
Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                   -09-252-991A-18053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-542-921-2
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RESULT 9

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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
359 LSNLQILVNYQTNGSAWRGSRVRYHYLHSSIIQEKSYGLLSDPVGANINVQNNDI 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---KAALRKAHTSMVRNFRYG---KPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%; Score 51; DB 2; Length 1169; 25.5%; Pred. No. 28; .ive 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: 1IZUKA, TOSHIHIKO
APPLICANT: ARAI, SATOSH
APPLICANT: ARAI, SATOSH
APPLICANT: MIZEKI, MASATSUGU
ITILE OF INVENTION: ONCEL BACILLUS STRAIN AND HARMFUL
ITILE OF INVENTION: ORGANISM CONTROLLING AGENTS
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCIFIIANN ...-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 2-JUN-1997
CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/542,921
FILING DATE: 11-OCT-1995
APPLICATION NUMBER: US 276082/94
FILING DATE: 14-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 49-209-0
TELEFRATION NUMBER: 49-209-0
TELEFRATION NUMBER: 107 24.618
REFERRENCE/DOCKET NUMBER: 49-209-0
TELEFRATION NUMBER: 107 2000
TELEFRAX: (703) 413-2200
TELEFRAX: (703) 413-2200
TELEFRAX: (703) 413-2200
TELEFRAX: 1070 IN 10
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5399, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF. 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                     Sequence 2, Application US/08880684
Patent No. 5837526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.5
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-107-532A-5399
                                                                                                                                                                                 US-08-880-684-2
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APPLICANT: Marc 1.

APPLICANT: Marc 1.

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS: TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE PERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18693

LENGTH: 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/05171
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.8%; Score 49.5; Dilarity 40.7%; Pred. No. 5.6; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...208
; SEQUENCE DESCRIPTION: SEQ ID NO: 5399:
US-09-107-532A-5399
                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Atiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOWNUNICATION INFORMATION:
TELEPHONE: (781)893-8277
TELEFRAK: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 NKAALRKAHTSMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 NKAA------QNFRYGKPFTPELE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18693, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                    ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                          COMPUTER: PC
OPERATING SYSTEM: <Unknown>
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 208 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5399
SEQUENCE CHARACTERISTICS:
                                              STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                       CITY: Waltham
                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Best Local Similarity
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US-09-252-991A-18693
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Job time
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     Gaps
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     15;
                                                                                                                                                                                                                                                        APPLICANT: van Slegtenhorst, Marjon
APPLICANT: Halley, Dicky
TITLE OF INVENTION: Compositions and Methods Based U
TITLE OF INVENTION: Sclerosis-1 (TSC-1) Gene and Gene Product
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                108 RMTANKPSIEQHKTLLEQ-RYDLSDRPAKGASMTRGKPLÓEGIRVK 153
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     9; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,708
FILING DATE:
CLASSIFICATION N.
ATTORNEY/AGENT INFORMATION:
NAME: SANIZO, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BRI331/42002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 639-6694
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49.5; DE
Pred. No. 48;
9; Mismatches
   11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              1455 Pennsylvania Avenue, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sampson, Julian R.
Povey, Sue
van Slegtenhorst, Marjon
Halley, Dicky
                                                                                                                                                                                                    Kwiatkowski, David J.
Sampson, Julian R.
Povey, Sue
Povey, Sue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kwiatkowski, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                STAIL.
COUNTRY. U.S.
ZIP. 20004-1008
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
TYPE: IBM PC compatible
TYPE: IBM PC compatible
TYPE: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09950046A Patent No. 6548258 GENERAL INFORMATION:
                                                                                                                                                    Sequence 2, Application US/09457708
Patent No. 6326483
                                   6 RILLNKAALRKAHTSMVRNFRY
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 22.8%;
Best Local Similarity 29.8%;
Matches 14; Conservative
12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     STREET: 1455
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STRANDEDNESS: not
TOPOLOGY: not rel
                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Kwiatk
                                                                                                                                                                                                                                                                                                                                                                                                   na.
D.C.
U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE: NO
US-09-457-708-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-09-950-046A-2
                                                                                                                                                                                                                        APPLICANT: APPLICANT:
                                                                                                                                    US-09-457-708-2
Matches
                                                                                                                    RESULT 14
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TITLE OF INVENTION: Compositions and Methods Based Upon the Tuberous Sclerosis-1 (TSC-1) Gene and Gene Product
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                      COUNTRY: U.S.

ZIP: 20004-1008
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/950,046A
FILLING DATE: 12-8P-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLSNLRILLNKAALRKAHTSMV----RNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                      NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BRI331/42002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49.5; DB
Pred. No. 48;
9; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 639-6585
TELEFAX: (202) 639-6604
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.8%; 29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 14; Conserv
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December 3, 2003, 14:32:37; Search time 30 Seconds (without alignments) 266.577 Million cell updates/sec
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217
1 MLSNLRILLNKAALRKAHTS......NFRYGKPVQSQVQLKPRDLC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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prodata/1/pubpaa/US10 NEW_PUB.pep:*
prodata/1/pubpaa/US60_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Segmental Co economical Segmental	Semience 1 Appli	Segmence 48 Appl	Semicon 54 Appl	K		άα	Semience 7915 An	Semience 7102 An	Semience 2 andi	Semience 46024 a	Semience 4869 An	Semience 10798	Segmence 3622 An	Sequence 4156, Ap	
SUMMARIES	US-08-765-244-22	US-08-765-244-1	US-10-061-395-48	US-10-052-942-54	US-09-998-027-3	US-10-165-099-3	US-10-353-856-8	US-10-156-761-7915	US-10-032-585-7102	US-09-950-046A-2	US-09-864-761-46024	US-09-815-242-4869	US-09-815-242-10798	US-09-738-626-3622	US-09-764-891-4156	
DB		8	14	15	11	12	12	15	7	10	6	σ	σ	10	11	
% Query Match Length DB	43	41	32	32	1286	1286	2212	414	564	1164	75	285	334	684	235	
% Query Match	100.0	8.06	42.4	42.4	28.1	28.1	23.3	23.0	23.0	22.8	22.4	22.4	22.4	22.4	22.1	
Score	217	197	92	92	61	61	50.5	20	50	49.5	48.5	48.5	48.5	48.5	48	
Result No.	н	7	m	4	Ŋ	9	7	6 0	σ	10	11	12	13	14	15	

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	10-061-201			5-247	7-627	1-627	1-962-16	-608	-685	4-761-3	-284-	-293-	-875	-878	0-270-786-27	0-710	-859	-846-2	-761	10-147-026-6	-752	-067B-	-762A	-078-10	1716-	-774	52	79	-730	-639
	0-061	0-063	0-032	9-756	35,	35	21	080	37	ŵ	-811-	0-177	0-270	0-270	0-270	0-270	0-270	0-270	0-156	0-147	9-881	9-986	-09-312-7	9-015	0-238	0-114	0-099	0-074	696-6	9-774
	US-1	US-1	US-1	7	US-1	US-1	US-10-	US-1	US-1	0S-09	US-09	US-1	US-10	_	7	1	_	US-1	US-1	US-1	US-0	US-0	US-0	US-0	US-1	US-1(US-1(9	0S-09
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1	22.1	22.1	22.1				21.4			21.2				21.0		21.0	21.0	21.0	21.0	21.0	20.7	20.7	20.7					20.5		20.3
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•	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

JS-08-765-244-22

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APPLICANT: Seibel, Peter
APPLICANT: Seibel, Andrea
TITLE OF INVENTION: FRAGMENT, PROCESS FOR PRODUCING THE SAME AND ITS USES FOR
TITLE OF INVENTION: APPROPRIATELY INTRODUCING NUCLEIC ACIDS INTO CELL ORGANELLES
TITLE OF INVENTION: AND CELLS
TITLE OF INVENTION: APPROPRIATELY INTRODUCING NUCLEIC ACIDS INTO CELL ORGANELLES
FILE REFERENCE: 1994-0018-999
CURRENT APPLICATION NUMBER: US/08/765,244
CURRENT PILING DATE: 1995-06-11
PRIOR FILING DATE: 1995-06-11
PRIOR FILING DATE: 1994-06-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PRESEQ FOR Windows Version 4.0
SEQ ID NO SEQ ID NOS: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLSNLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDLC 43
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Sequence 22, Application US/08765244
Publication No. US20010008771A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Rattus rattus
US-08-765-244-22
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RESULT 2 US-08-765-244-1 ; Sequence 1, Application US/08765244

US20010008771A1

Publication No.

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APPLICANT: Zauderer, Maurice
APPLICANT: Smith, Ernest
APPLICANT: Wei, Chungwen
TILE OF INVENTION: Methods of Producing or Identifying Intrabodies in Eukaryotic C
FILE SPERENCE: 1821.009004
CURRENT APPLICATION NUMBER: 05/298,095
PRIOR APPLICATION NUMBER: 60/298,095
PRIOR APPLICATION NUMBER: 60/298,095
PRIOR APPLICATION NUMBER: 60/271,422
PRIOR APPLICATION NUMBER: 60/263,200
PRIOR FILING DATE: 2001-02-27
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin version 3.0
SEQ ID NO 54
LENGTH: 22
THENGTH: 22
THENGTH: 22
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Publication No. US20030093819A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: D'Andrea et al.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Diagnosis and Treatment of Cancers Associated with Defective
FILE REFERENCE: 2486/101
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OTHER INFORMATION: signal sequence
NAME/KEY. UNBURE

COTHER INFORMATION: Xaa may represent any amino acid
NAME/KEY: UNBURE

INFORMATION: Xaa may represent any amino acid
NAME/KEY: UNBURE

COCATION: (32). (32)

OTHER INFORMATION: Xaa may represent any amino acid
US-10-052-942-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42,4%; Score 92; DB 15; 61.3%; Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
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CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1286
                                                               Sequence 54, Application US/10052942
Publication No. US20030104402A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i LOCATION: (1)...(1286)
; OTHER INFORMATION: Plantfancd2
US-09-998-027-3
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 61.3;
Matches 19; Conservative
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ORGANISM: A. thaliana
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Best Local Similarity
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NAME/KEY: PEPTIDE
                                            -10-052-942-54
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APPLICANT: Seibel, Peter
APPLICANT: Seibel, Andrea
APPLICANT: Seibel, Andrea
ATILE OF INVENTION: CHIMERICAL PEPTIDE-NUCLEIC ACID
TITLE OF INVENTION: PRAGMENT, PROCESS FOR PRODUCING THE SAME AND ITS USES FOR
TITLE OF INVENTION: AND CELLS
TITLE OF INVENTION: DATE: 1997-06-10
PRIOR APPLICATION NUMBER: DCT/DE95/00775
PRIOR APPLICATION NUMBER: DCT/DE95/00775
PRIOR APPLICATION NUMBER: DCT/DE95/00775
PRIOR PELLING DATE: 1994-06-16
NUMBER OF SEQ ID NOS: 22
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Heterologous signal sequence for the mitochondrial matrix NAME/KEY: MISC FEATURE LOCATION: (7). (8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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US-10-061-395-49

i Sequence 48. Application US/10061395
i Publication No. US20020192675A1
i GENERAL INFORMATION:
APPLICAMT: Smith, Enest S.
ITILE OF INVENTION: Methods of Identifying Regulator Molecules
FILE REFERENCE: 1821.0080003
CURRENT APPLICATION NUMBER: US/10/061,395
CURRENT APPLICATION NUMBER: 60/271,423
PRIOR PLILING DATE: 2001-02-04
PRIOR PLILING DATE: 2001-02-07
PRIOR PLILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 116
SSEQ ID NO 48
LENGTH: 32
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Pred. No. 3.7e-22;
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) OTHER INPORMATION: May be any amino acid
US-10-061-395-48
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NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.8%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 61.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-765-244-1
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APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7102
LENGTH: 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 LSDLELLIVIAAVRMIEKFELQTINFNLAYTEYQEMVKNFNTGNAIVSSTSLDSR 478
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Pred. No. 77;
6; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 RILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPR
Sequence 7915, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, UUN
APPLICANT: ISHIKAWA, UUN
APPLICANT: SHIKAWA, UUN
APPLICANT: SHIKAWA, UND
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPRENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US/2001-204089
PRIOR PILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.0%; Score 50; Best Local Similarity 34.3%; Pred. No. 9 Matches 12; Conservative 5; Mismatch
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Povey, Sue
van Slegtenhorst, Marjon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7102, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 29.1%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LSNLRILLNKAALR-
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                                                                                                                                                                                                    Publication No. US20030188326A1

Publication No. US20030188326A1

Publication No. US20030188326A1

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS OF CANCER SUSCEPTIBILI

TITLE OF INVENTION: DEFECTIVE DNA REPAIR MECHANISMS AND TREATMENT THEREOF

CURRENT APPLICATION NUMBER: US/10/165,099

CURRENT APPLICATION NUMBER: US 09/998,027

PRIOR FILING DATE: 2001-11-02

PRIOR FILING DATE: 2000-11-03

PRIOR SELING DATE: 2000-11-03

NUMBER OF SEQ ID NOS: 352

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kawacka, Yoshihiro
APPLICANT: Jasenosky, Luke D.
APPLICANT: Jasenosky, Luke D.
APPLICANT: Wisconain Gabriele
APPLICANT: Wisconain Alumni Research Foundation
TITLE OF INVENTION: Filovirus Vectors and No. US20030215794Alinfectious Filovirus-Base
TITLE REPRENCE: 800.033USI.
CURRENT APPLICATION NUMBER: US/10/353,856
PRIOR APPLICATION NUMBER: US 60/353,972
PRIOR FILING DATE: 2002-01-31
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         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.1%; Score 61; DB 12; Length 1286; 38.2%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 VINDLRELISNRRLKDYQQEKIRDFH---KILLQLQLSPQQFC 366
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    14;
                                                                         ||||| :|: :: | |:||| |:| |:| swlrrmlssssttkrdeslyrnlllyspiqldig 140
                                                 3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
    7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/10353856; Publication No. US20030215794A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Reston Ebola virus
US-10-353-856-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 38.2
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-10-156-761-7915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1286
                                                                                                                                                                                     US-10-165-099-3
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Matches
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us-08-765-244-22.rapb

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22.4%; Score 48.5; DB 9; Length 75; 40.0%; Pred. No. 12; ive 3; Mismatches 11; Indels
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APPLICANT: Chise, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawich, Judith W.
APPLICANT: Trawich, John D.
APPLICANT: Trawich, John D.
APPLICANT: Trawich, Robert T.
APPLICANT: Amamorch, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFREENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2000-03-21
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR FILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR FILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR FILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: 60/207,727
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
OTHER INFORMATION: SWISSPROT HIT: P16960, EVALUE 3.00e-27
                                   FRICK FILING DATE: 2001-01-30

PRICK FILING DATE: 2001-01-30

PRICK PILING DATE: 2001-01-30

PRICK PILING DATE: 2001-01-30

PRICK PILING DATE: 2001-01-30

PRICK FILING DATE: 2001-01-30

PRICK FILING DATE: 2001-01-30

PRICK FILING DATE: 2001-01-30

PRICK PILING DATE: 2001-01-30

PRICK APPLICATION NUMBER: PCT/US01/00665

PRICK APPLICATION NUMBER: PCT/US01/00668

PRICK APPLICATION NUMBER: PCT/US01/00663

PRICK APPLICATION NUMBER: PCT/US01/00663

PRICK APPLICATION NUMBER: PCT/US01/00661

PRICK APPLICATION NUMBER: PCT/US01/00661

PRICK APPLICATION NUMBER: PCT/US01/00661

PRICK APPLICATION NUMBER: PCT/US01/00661

PRICK APPLICATION NUMBER: US 09/608,408

PRICK APPLICATION NUMBER: US 09/608,408

PRICK APPLICATION NUMBER: US 09/774,203

PRICK PILING DATE: 2000-06-30

PRICK PILING DATE: 2000-06-30

PRICK PILING DATE: 2000-06-30

PRICK PILING DATE: 2000-06-30

PRICK PILING DATE: 2001-01-29

PRICK 
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Patent No. US20020061569A1
GENERAL INPORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 40.0
Matches 14; Conservative
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Patent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
Halley, Dicky
TITLE OF INVENTION: Compositions and Methods Based Upon the Tuberous
Sclerosis-1 (TSC-1) Gene and Gene Product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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22.8%; Score 49.5; DB 10; Length 1164;
Best Local Similarity 29.8%; Pred. No. 2.2e+02;
Matches 14; Conservative 9; Mismatches 19; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLSNLRILLNKAALRKAHTSWV-----RNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC_COMPATIBLE
COMPUTER: IBM PC_DOS/MS-DOS
OFFRARING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/950,046A
FILING DATE: 12-Sep-2001
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BRI331/42002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-6585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REPERRICE: Acondours. CENERALION ANALISES
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PELING DATE: 2001-05-23
PRIOR PELING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-36
PRIOR PLING DATE: 2000-01-04
PRIOR PILING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PURGES
PRIOR PELING DATE: 2000-09-27
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STRANDENBESS: not relevant
TOPCLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                           CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20004-1008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 639-6604 INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                 NUMBER OF SEQUENCES: 28
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US-09-864-761-46024
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yangunco, Robert T.
APPLICANT: Yangunco, Robert T.
APPLICANT: Yangunco, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryces
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/918,078
PRIOR PELING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLILING DATE: 2000-12-16
PRIOR PLILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2010-02-16
PRIOR FILING DATE: 2010-02-16
PRIOR FILING DATE: 2010-02-16
SOFTWARE: PASESEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10798, Application US/09815242
Patent No. US20020661569A1
GAPBRAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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US-09-815-242-10798
                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Enterococcus faecalis US-09-815-242-4869
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Best Local Similarity
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LENGTH: 334
                                                                                                                                                                                                                                                                              SEQ ID NO 4869
LENGTH: 285
TYPE: PRT
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LOCATION: (221)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (208)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Mucleic Acids, Proteins, and Antibodies FILE REFERENCE: PCOO.
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4156
LENGTH: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 NSLHVLRNGSDILRRNEHHCWVFENF--NKPIDPPVRLGPRDI 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR FILING DATE: 1999-12-16

PRIOR PLING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR PLING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: JP 00/280988

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SEQ ID NO 3622

LENGTH: 684

TAVED: ....
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4156, Application US/09764891; Publication No. US20030077808A1; GENERAL INFORWATION:
                                                    Sequence 3622, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                       APPLICANT: ANDOGUCHI, HINGSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HANGSHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NACKO
APPLICANT: TATEISHI, NACKO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
                                                                                                                                      APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (228)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
RESULT 14
US-09-738-626-3622
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3 14:51:10 2003
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    i LOCATION: (221)
    i OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
    i LOCATION: (234)
    i COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-4156
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0; Gaps Query Match
22.1%; Score 48; DB 11; Length 235;
Best Local Similarity 37.0%; Pred. No. 54;
Matches 10; Conservative 7; Mismatches 10; Indels ò

0

Search completed: December 3, 2003, 14:35:35 Job time : 30 secs

qq

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 3, 2003, 14:30:02 ; Search time 21 Seconds (without alignments) 196.917 Million cell updates/sec

Run on:

US-08-765-244-22 Title:

1 MLSNLRILLNKAALRKAHTS........NFRYGKPVQSQVQLKPRDLC 43 Perfect score: Sequence:

283308 segs, 96168682 residues Searched:

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ornithine carbamoy	ornithine carbamoy	ornithine carbamoy	ornithine transcar	hypothetical prote	Gre binding conser	ornithine carbamoy	F16F4,13 protein -	ornithine transcar	hypothetical prote	oxygen-independent	chromokinesin - ch	sensor-like protei	cyclin B5 - yeast	nitrate/nitrite se	nitrate/nitrite se	translation elonga	probable two-compo	hypothetical prote	nitrate/nitrite se	nitrate/nitrite se	nitrate/nitrite se	hypothetical prote	WD-repeat protein	nitrate/nitrite se	hypothetical prote		hypothetical prote	
SUMMARIES	ID	OWRT	OWING	OWEU	I52779	B71413	F90409	JE0309	A86345	A48421	T32702	AD0950	A56514	140646	831290	T47000	AB0239			_				G70233			S76749	S545	T231	
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*	Query	91.7	75.6	65.0	54.8	28.1	27.6	26.3	25.6	25.3	24.9	24.9	24.9	24.7	24.4	24.4	24.4	24.2	4	24.0	4	24.0	4	23.7	23.5	'n	m,	23.5	23.5	23.3
	Score	199	164	141	119	61	9	57	55.5	52	Ω 4	54	54	53.5	23	53		52.5	52	52	52	52	S	51.5	51	51	51		51	50.5
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short-chain-specif	himothetical prote	hypothetical prote	mots homolog lafu	CAAX prenyl protei	probable molybdopt	signal recognition	calcium-dependent	cytochrome c PA303	purine NTPase [imp	tumor suppressor p	18c protein (clone	· hypothetical prote	GTP-binding protei	conserved hypothet
B83922 E90267	081100	H86026	F40590	H75127	F72773	A58947	AB1979	G83266	B90395	T03814	S57240	T33068	B69518	C81719
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ALIGNMENTS

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ornithine carbamoyltransferase (EC 2.1.3.3) precursor - rat
N;Alternate names: citrulline phosphorylase; ornithine transcarbamylase
C;Specias: Ratus norvegicus (Norway rat)
C;Date: 28-Feb-1986 #sequence revision 28-Feb-1986 #text change 11-Jun-1999
C;Accession: A00563; A28042; A23090; S02466; I52976; I67609; I53457
F;Taktyguchi, M.; Miura, S.; Mori, M.; Tatibana, M.; Nagata, S.; Kaziro, Y.
Proc. Natl. Acad. Sci. U.S.A. 81, 7412-7416, 1984
A;Title: Molecular cloning and nucleotide sequence of cDNA for rat ornithine carbamoyl
A;Reference number: A00563; MUID:85063800; FMID:6095294

A; Accession: A00563

A; Molecule type: mRNA
A; Residues: 1-354 < TAKI>
A; Residues: 1-354 < TAKI>
A; Cross-references: GB: K03040; NID: 9205873; PIDN: AAA41768.1; PID: 9205874
A; Cross-references: GB: K03040; NiD: Apric, M.
B; Takiguchi, M.; Murakani, T.; Miura, S.; Mori, M.
Proc. Natl. Acad. Sci. U.S.A. 84, 6136-6140, 1987
A; Title: Structure of the rat ornithine carbamoyltransferase gene, a large, X chromosc A; Reference number: A28042; MUID: 87317609; PMID: 3476935

A; Accession: A28042

A, Molecule type: DNA A; Residues: 1-344 cTMZ> A; Residues: 1-344 cTMZ> A; Cross-references: GB:MA6933; GB:J02957; NID:g205884; PIDN:AAA41769.1; PID:g205886 A; Kraus, J.P.; Hodges, P.E.; Williamson, C.L.; Horwich, A.L.; Kalousek, F.; Williams, Nucleich Acids Res. 13, 943-952, 1985 Nucleich Acids Res. 13, 943-952, 1985 A; Title: A cDNA clone for the precursor of rat mitochondrial ornithine transcarbamylas A; Reference number: A23090; WUID:85215524; PMID:3839075

A; Accession: A23090

A;Molecule type: mRNA
A;Residues: 1-38,'P',40-240,'S',242-354 <KRA>
A;Residues: 1-38,'P',40-240,'S',242-354 <KRA>
A;Cross-references: GB:X01976
B;Aoki, Y.; Sunaga, H.; Suzuki, K.T.
Biochem. J. 250, 735-742, 1988
A;Title: A cadmium-binding protein in rat liver identified as ornithine carbamoyltrans
A;Reference number: 802466; MUID:88268748; PMID:3390141
A;Accession: 802466

A;Molecule type: protein A;Residues: 33-56;293-302;307-317;322-329 <AOK> R;MCIntyre, P.; Graf, L.; Mercer, J.F.B.; Wake, S.A.; Hudson, P.J.; Hoogenraad, N. DNA 4, 147-156, 1985

A;Title: The primary structure of the imported mitochondrial protein, ornithine transc A;Reference number: 152976; MUID:85203360; PMID:3838931
A;Accession: 152976
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>

A;Cross-references: GB:M11266; NID:9205871; PIDN:AAA41767.1; PID:9205872
R;McIntyre, P.; Graf, L.; Mercer, J.; Peterson, G.; Hudson, P.J.; Hoogenraad, N.
FBBS Lett. 177, 41-46, 1984
A;Title: A highly basic N-terminal extension of the mitochondrial matrix enzyme ornit?
A;Reference number: I53457; MUID:85051832; PMID:6548714

Query Match

셤 ò

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A,Molecule type: DNA
A,Residues: 'M',33-100,'F',102-110,'P',112-192,'CF',195-269,'R',271-354 <WHE>
A,Rote: this report represents a synthetic gene designed for expression in (rather tha R,Horwich, A.L., Kalousek, F', Rosenberg, L.E.
Proc. Natl. Acad. Sci. U.S.A. 82, 4930-4933, 1985
A,Title: Arginine in the leader peptide is required for both import and proteolytic clayReference number: I59039; MUID:85270440; PMID:3895227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1.36 kBE2-
A; Cross-references: GB2-
A; Cross-references: GB2-
A; Cross-references: GB2-
B; Gilbert-Dussardier, B.; Rabier, D.; Strautnieks, S.; Segues, B.; Bonnefont, J.P.; Mu
Hum. Mol. Genet. 3, 831-832, 1994
A; Title: A novel arginine (245) to glutamine change in exon 8 of the ornithine carbamo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 26-276, 'Q', 278-289 <RE3>
A; Cross-references: GB:S73640; NID:g688001; PIDN:AAB31859.1; PID:g688002
A;Note: this sequence represents a disease defect in ornithine carbamoyltransferase C; Comment: The active enzyme is a dimer of identical chains with one tightly bound zin
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Kraus, J.P.; Doolittle,
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R;Wheeler, V.C.; Prodromou, C.P.; Pearl, L.H.; Williamson, R.; Coutelle, C.
Gene 169, 251-255, 1996
A;Title: Synthesis of a modified gene encoding human ornithine transcarbamylase for
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: citrulline phosphorylase; conithine transcarbamylase C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A41444; B41444; A00562; 138078; JC4672; I59039; I54377
R;Hata, A.; Tsuzuki, T.; Shimada, K.; Takiguchi, M.; Mori, M.; Matsuda, I. J. Biochem. 103, 302-308, 1988
A;File: Structure of the human ornithine transcarbamylase gene.
A;Reference number: A41444; MUID:88227905; PMID:2836378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hata, A.; Tsuzuki, T.; Shimada, K.; Takiguchi, M.; Mori, M.; Matsuda, I..
Biochem. 100, 717-725, 1986
Title: Isolation and characterization of the human ornithine transcarbam.
                             Gaps
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;Residues: 1-100,'F',102-110,'P',112-192,'CF',195-269,'R',271-354 <HOR>
;Cross-references: GB:D00230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Residues: 1-354 < HAI> | Cross-references: GB: D00230; NID: 9219957; PIDN: BAA00161.1; PID: 9219959
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                         Indels
                                                                                                                                                                                                                                                                                                                                     ornithine carbamoyltransferase (EC 2.1.3.3) precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GB:D00230, NID:g219957; PIDN:BAA00161.1, R;Horwich, A.L., Fenton, W.A.; Williams, K.R.; Kalousek, F.; Science 224, 1068-1074, 1984
A;Fitle: Structure and expression of a complementary DNA for A;Reference number: A00562; WUID:84196410; PMID:6372096
                                                                                                                             1 MLSNLRILIANNAALRKGHTSVVRHFWCGKPVQSQVQLKGRDL
                                                                                        1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL
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                         5,
                  Mismatches
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A;Status: translated from GB/EMBL/DDBJ
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                      5,
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                  Conservative
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Residues: 1-26 <RES>
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                  35;
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A;Note: the end of this sequence is near the boundary of the cloned region and may be ar
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                    Aintrons: 26/2, 72/3; 100/1; 129/2; 180/3; 221/3; 239/3; 289/3; 335/3
C;Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
C;Superfamily: ornithine carbamoyltransferase; mitochondrion; transferase; urea cycle
F;1-32/Domain: transit peptide (mitochondrion) #status predicted <TMP>
F;33-354/Product: ornithine carbamoyltransferase #status predicted <MAT>
F;40-342/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the ornithine transcarbamylase gene contains DNA sequ
6224037; PMID:3011788
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A;Introns: 26/2; 72/3; 100/1; 129/2; 180/3; 221/3; 239/3; 289/3
C;Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
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Science 237, 415-417, 1987
A/Title: The molecular basis of the sparse fur mouse mutation.
A/Reference number: A43609; MUD:87263407; PMID:3603027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                       A;Cross-references: EMBL:X01178; NID:956802; PIDN:CAA25618.1; PID:956803
A;Accession: 153457
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-43, N',45-99,'R',101-102 <RB3>
A;Cross-references: GB:K03041; NID:9205889; PIDN:AAA41771.1; PID:9205890
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-354 «VER.»
A;Cross-references: GB:M17030; NID:g200162; PIDN:AAA39865.1; PID:g200163
R;Scherer, S.E.; Veres, G.; Caskey, C.T.
Rvoleic Acids Res. 16, 1593-1601, 1988
A;Title: The genetic structure of mouse ornithine transcarbamylase.
A;Reference number: S03407; MUID:88157717; PMID:2831503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ornithine carbamcyltransferase (EC 2.1.3.3) precursor - mouse N;Alternate names: citrulline phosphorylase; ornithine transcarbamylase C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1993 #sequence_revision 13-Mar-1703 #sequence_revision 13-Mar-1703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Cross-references: EMBL:X07092
R.Vores, G., Craigen, W.J., Caskey, C.T.
J. Biol. Cham. 261, 7588-7591, 1986
A.Title: The 5' Elanking region of the ornithine transcarbamyl
A.Reference number: 155252; MUID:86224037; PMID:3011788
A.Accession: 155252
A.Status: translation not shown; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.7%; Score 199; DB 1; 97.6%; Pred. No. 9.3e-20;
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-102 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 164; DB 1;
Pred. No. 6.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keywords: mitochondrion; transferase; urea cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-194,'R',196-335 <SCH>
Cross-references: EMBL:X07092
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: translation not shown
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Matches 41; Conserv
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Best Local Similarity
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Gene: OIC

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C; Species: Sulfolobus soffataricus
C; Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C; Accession: F90409
C; Accession: F90409
R; She, Q: Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Che Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                    GTP binding conserved hypothetical protein SSO2385 [imported] - Sulfolobus solfatariou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structure, regulation, and chromosom
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C;Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE006641; NID:g13815687; PIDN:AAK42533.1; GSPDB:GN00155
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: transferase
F;40-342/Domain: aspartate/ornithine carbamoyltransferase homology <AOC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 ILLINKAA-----LRKAHTSMVRNFRY----GKPVQSQVQ-----LKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Gallus gallus (chicken)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 351;
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S;Shimogizi, T.; Kono, M.; Mannen, H.; Mizutani, M.; Tsuji, J. Biochem. 124, 962-971, 1998
A;Title: Chicken ornithine transcarbamylase gene, structure, A;Reference number: JE0309; MUID:99011321; PMID:9792920
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                                                                                                                                                                           36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                             Similarity 38.2%; Pred. No. 5.2; 13; Conservative 7; Mismatches
                                                                                                                               3 SNLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60; DB 2
Pred. No. 1.7;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57; DB 2
Pred. No. 4.5;
4; Mismatches
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Best Local Similarity 40.57
Matches 17; Conservative
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Best Local Similarity 34.6:
Matches 18; Conservative
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A, Accession: F90409
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A,Residues: 1-351 <KUR>
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A, Status: preliminary
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                                                              13;
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                                Best Local
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e synthesis of UMP.
C;Comment: The active enzyme catalyzes the condensation of carbamoyl phosphate and ornit C;Comment: The active enzyme catalyzes the condensation of carbamoyl phosphate and ornit A;Genetics GDB:U19468; OMIM:311250
A;Cross-references: GDB:119468; OMIM:311250
A;Map position: Yp21.1.**
A;Map position: Yp21.1.**
A;Map position: Yp21.1.**
A;Map position: Appl.1.**
C;Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
C;Keywords: arginine biosynthesis; homotrimer; mitochondrion; transferase; urea cycle F;1-32/Domain: transit peptide (mitochondrion) #status predicted <NMP>
F;33-354/Product: ornithine carbamoyltransferase #status predicted <MAT>
F;40-342/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Day
C;Accession: B71413
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A/Molecule type: DNA
A/Molecule type: DNA
A/Residucus: 1-41 < RES>
A/Cross-references: GB:ML2583; NID:g205887; PIDN:AAA41770.1; PID:g205888
C/Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
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A; Accession: B71413
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLFNLRILLNNAAFRNGHNFMVRNFRCGQPLQNKVQLKGRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLSNIRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 119; DB 2; Len
Pred. No. 1.1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 141; DB 1;
Pred. No. 1e-11;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ornithine transcarbamylase peptide - rat (fragment)
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Best Local Similarity 69.0%;
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 4COP9-4G3845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-1286 <BEV>
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Best Loca Matches

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R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churche th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser A;Reference number: ABOSO2; MUID:21534947; PMID:11677608
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cipedcies: Gallus gallus (chicken)
Cipate: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 02-Feb-2001
Airitle: Chromokinesin: a DNA-binding, kinesin-like muclear protein.
Airitle: Chromokinesin: a DNA-binding, kinesin-like muclear protein.
Airitle: Reference number: A56514; MUD:95181533; PMID:7876303
Airitle: Adder, R.
Airitle: Adder, R.
Airitle: Adder, R.
Airitle: Adder, R.
Airitle: A developmentally regulated basic-leucine zipper-like gene and its expression
Airitle: Advelopmentally regulated basic-leucine zipper-like gene and its expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Salmonella enterica sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-457 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03096.1; PID:g16504733; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oxygen-independent coproporphyrinogen III oxidase [imported] - Salmonella er C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AD0950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: U04821; NID: 9440792; PIDN: AAA18960.1; PID: 9440793
                                                                                                                                                                                                                                                                                                                                                                           Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                            A,Gene: CESP:C14C6.13
A,Map position: 5
A;Introns: 91/1; 129/2; 145/3; 267/3
C,Superfamily: Caenorhabditis elegans hypothetical protein C14C6.13
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                                                                                                                                                                                                                                                                        Query Match 24.9%; Score 54; DB 2; Length 300; Best Local Similarity 31.4%; Pred. No. 9.9; Matches 11; Conservative 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.9%; Score 54; DB 2; Length 457; 26.5%; Pred. No. 16; ive 10; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Superfamily: oxygen-independent coproporphyrinogen oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LSNLRILLNKAALRKAHTSMVRNFRYGKPVOSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||| : : | : || : || : || : || : || 118 || LINKAQISRLMTLLRENFHFNTDAEISIEVDPREI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 728-1086, RI' <WA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
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Best Local Similarity
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                     C;Genetics
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Cornithine transcarbamylase - bullfrog
Cornithine 
ansen, N.F.; Hughes, B.; Huizar, L.

Atture 408, 816-820, 2000

A, Authors: Hunter, J.L.; Jenonson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
A; Zzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Titles: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: liver
A; Note: sequence extracted from NCBI backbone (NCBIN:126154, NCBIP:126155)
C; Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-300 <DAV>
A;Cross-references: EMBL:AF039051; PIDN:AAB94269.1; GSPDB:GN00023; CESP:C14C6.13
A;Experimental source: strain Bristol N2; clone C14C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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C;Genetics:
A;Map position: 1
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A; Residues: 1-350 <HEL>
A; Cross-references: GB:M95193; NID:g213683; PIDN:AAA49528.1; PID:g213684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: Orniums construction C; Keywords: mitochondrion
C; Keywords: mitochondrion
F; 36-338/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55.5; DB 2;
Pred. No. 9.6;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     422 KAAYSRISIDSPSRNYRESQPMGSPVQARPR 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.6
Best Local Similarity 45.2
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Accession: A48421
A, Status: preliminary
A, Molecule type: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-454 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-435 < COH>
A;Cross-references: EMBL:U40828; NID:g1066467; PIDN:AAB68061.1; PID:g1066475; MIPS:YPF
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiBuchrieser, C.; Rusniok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; Carni submitted to the EMBL Data Library, October 1998
A;Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: 17,000
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-593 < BUC>
A; Experimental source: strain 6/69
C; Superfamily: nitrate/nitrite sensor protein narX
C; Reywords: autophosphorylation; phosphohistidine; phosphoprotein; phosphotransferase; F; 401/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Yersinia pestis
C.Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nitrate/nitrite sensor protein (EC 2.7.3.-) [similarity] - Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                        24.4%; Score 53; DB 2; Length 435; 46.4%; Pred. No. 20; tive 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match . 24.4%; Score 53; DB 2; Length 593; Best Local Similarity 34.1%; Pred. No. 29; Matches 14; Conservative 8; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLSNLRILLNKAALRKAHTSMVRNF--RYGKPVQSQVQLKP 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNLKILQNKRALSKNDSSSKQQVQDSKP
                                                                                                                                                              A)Gene: SGD:CLB5, CLB5
A)Cross-references: SGD:S0006324
A)Map position: 16R
C;Superfamily: cyclin
C;Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 13; Conserv
                         A;Accession: S69013
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A; Residues: 1-435 < EBS>
A; Residues: 1-435 < EBS>
A; Cross-references: EBSI-M91209; NID:g171238; PIDN:AAA34503.1; PID:g171239
B; Schwob, E.; Naemyth, K.
Genes Dev. 7, 1160-1175, 1993
A; Title: CLB5 and CLB6, a new pair of B cyclins involved in DNA replication in Saccharom A; Reference number: S36228; MUID:93307652; PMID:8319908
A; Reference number: acid sequence not shown
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: envZ protein; sensor histidine kinase homology
C;Keywords: autophosphorylation; phosphohistidine; phosphoprotein
F;196-421/Domain: sensor histidine kinase homology <SHK>
F;227/Binding site: phosphate (His) (covalent) (by autophosphorylation) #status predicte
C;Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology C;Keywords: ATP; DNA binding; mitosis; nucleotide binding; P-loop F;11-344/Domain: kinesin motor domain homology <KMOT> F;88-95/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sensor-like protein - Coxiella burnetii
C;Species: Coxiella burnetii
C;Species: Coxiella burnetii
C;Species: L2-May-1996 #sequence_revision 12-Aug-1996 #text_change 31-Mar-2000
C;Accession: 140646
R;Mo, Y.Y.; Mallavia, L.P.
Gene 151, 185-190, 1994
A;Title: A coxiella burnetii gene encodes a sensor-like protein.
A;Reference number: 140646; MUID:95129857; PMID:7828872
A;Accession: 140646; MUID:95129857; PMID:7828872
A;Accession: 140646
A;Molecule type: DNA
A;Residues: 1-425 cRES>
A;Cessidues: BMBL:U07186; NID:9460628; PIDN:AAA81939.1; PID:9460629
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$31290
Gyolin B5 - yeast (Saccharomyces cerevisiae)
Nylletmate names: protein P9642 8; protein YPR120c
C;Species: Saccharomyces cerevisiae
C;bate: 28 May-1993 #sequence revision 28-May-1993 #text_change 19-Apr-2002
C;Accession: 531290; Sego13
R;Epstein, C.B.; Cross, P.R.
Genes Dev. 6, 1695-1706, 1992
A;Title: CLB5: a novel B cyclin from budding yeast with a role in S phase.
A;Reference number: $31290; MUD:92387544; PMID:1387626
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A;Cross-references: EMBL:X70435; NID:g396496; PIDN:CAA49893.1; PID:g396497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                    DB 2; Length 1225;
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                                                                                                                                                              Score 54; DB 2; Length 122
Pred. No. 46;
9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                         2 LSNLRILLNKA-ALRKA-HTSMVRNFRYGKPVQSQVQLKPRDL 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 IKILGRASALKRAFTNLLNNAIRYAKNVNVRIQ 343
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                                                                                                                                                                 24.9%;
39.5%;
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Best Local Similarity 39.5'
Matches 17; Conservative
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Matches 12; Conservative
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Gaps

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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sw model using protein search,

December Run on:

3, 2003, 14:17:57; Search time 11 Seconds (without alignments)
183.832 Million cell updates/sec

US-08-765-244-22

21.7 1 MLSNLRILLNKAALRKAHTS.....NFRYGKPVQSQVQLKPRDLC Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cripti	P00481 rattus norv	P11725 mus musculu		metha	Q8pu78 methanosarc	P31326 rana catesb	Q9bbs6 lotus japon					Ogpkr6 chlamydia m		Q09855 schizosacch	saccharon					-	sulfolopo	Q9z136 rattus norv		P32131 escherichia	Q04439 saccharomyc	P38800 saccharomyc	P16960 sus scrofa	P11716 oryctolagus	7	σ	P59483 buchnera ap	5 anabaena	P00723 kluyveromyc
SUMMARIES	ID	OTC RAT	OTC_MOUSE	OTC HUMAN	IF2P METAC	IF2P_METMA	OTC RANCA	RR2_LOTJA	HEMN SALTY	KF4A_CHICK	OTC_PIG	CGSS YEAST	EFP1 CHLMU	NARX ECOLI	POFB_SCHPO	YM37_YEAST	C9DA_BACTP	TRB2_SULSO	LAFU_VIBPA	SR68_CANFA	PRCA_ANASP	RAS0_SULSO	TSC1 RAT	TSC1_HUMAN	HEMN ECOLI	MYS5_YEAST		RYR1_PIG		RYR1_HUMAN	er:	SYR_BUCBP	- 1	BGAL_KLULA
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ø	Query Match	91.7	75.6	65.0	27.2	25.8	25.3	24.9	24.9	24.9		24.4	24.2	24.0	23.5	23.5	23.5	23.3	23.0	23.0	23.0	22.8	22.8	22.8	22.6	22.6	22.6	22.4		22.4	22.1	22.1		22.1
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Y376_BUCAP OVOS_CHICK	RRPL_EBOSM R37B_SCHPO	PSMA_PYRAB	PSMA_PYRHO	TES HUMAN	TES_MOUSE	RPOP MAIZE	T801 PSESH	VCOM ADECC	VCOM_ADECR
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3.4 3.5	36	38	გ	40	41	42	43	44	45

ALIGNMENTS

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-!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
                                                                                                                                                                                                 Rattus norvegicus (Rat).
Bukaryota, Metacoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-85215524; PubMed=3839075; Kraus J.P., Kalousek F., Kraus J.P., Hodges P.E., Williamson C.L., Horwich A.L., Kalousek F., Williams K.R., Rosenberg L.E.; Williams K.R., Rosenberg L.E.; A cDNA clone for the precursor of rat mitochondrial ornithine transcarbamylase: comparison of rat and human leader sequences and conservation of catalytic sites."; Nucleic Acids Res. 13:943-952(1985).
                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ocntithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
(OTGase) (Ornithine transcarbamylase).
                                                                                                                                                                                                                                                                                                                                                                                  Takiguchi M., Murakami T., Miura S., Mori M.; "Structure of the rat ornithine carbamcyltransferase gene, a large, chromosome-linked gene with an atypical promoter."; proc. Natl. Acad. Sci. U.S.A. 84:6136-6140(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88268748; PubMed=3390141;
Aoki Y., Sunaga H., Suzuki K.T.;
"A cadmium-binding protein in rat liver identified as ornithine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The primary structure of the imported mitochondrial protein, ornithine transcarbamylase from rat liver: mRNA levels during ontogenv.";
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McIntyre P., Graf L., Mercer J.F.B., Wake S.A., Hudson P.J.,
Hoogenraad N.;
                                                                                                                                                                                                                                                                                   carbamoyltransferase precursor.";
Proc. Natl. Acad. Sci. U.S.A. 81:7412-7416(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [5]
SEQUENCE OF 33-56; 293-302; 307-317 AND 321-329.
 354 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                 STRAIN-Wistar; TISSUE-Liver;
MEDLINE-87317609; PubMed-3476935;
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SEQUENCE FROM N.A.
               P00481; Q63407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Veres G., Craigen W.J., Caskey C.T.,
"The 5' flanking region of the ornithine transcarbamylase gene
ontains DNA sequences regulating tissue-specific expression.";
J. Biol. Chem. 261:7588-7591(1986).
i. CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHRAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
-!- SUBUNIT: Homotrimer.
-!- SUBCELLULAR LOCATION. Mitochondrial matrix.
-!- DISEASE: SPARSE FUR (SPF) MOUSE HAVE AN OTC WITH AN OVERALL DECREASE IN ACTIVITY, AND ALTERED SUBSTRATE AFFINITY.
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
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InterPro; IPR006130; Asp/Orn_Cotranf.
InterPro; IPR006131; Ord.
InterPro; IPR00185; Ord.
InterPro; IPR000685; Ord.
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ONLITHINE CARBAMOYLTRANSFERASE.
BY SIMILARITY.
BY SIMILARITY.
F > N (IN SPARSE FUR MOUSE).
G -> R (IN REF. 2).
W, 33BBEDIE88AA196 CRC64;
                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE EROM N.A.
MEDLINE=8815717; PubMed=2831503;
Scherer S.E., Veres G., Caskey C.T.;
Scherer S.E., Veres G. mouse ornithine transcarbamylase.";
Whe genetic structure of mouse ornithine transcarbamylase.";
Nucleic Acids Res. 16:1593-1601(1988).
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                        Veres G., Gibbs R.A., Scherer S.E., Caskey C.T., "The molecular basis of the sparse fur mouse mutation."; Science 237:415-417(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M17030; AAA39865.1; -...
EMBL; M12716; AAA39865.1; -...
EMBL; X07092; CAA30121.1; JOINED.
EMBL; X07094; CAA30121.1; JOINED.
EMBL; X07094; CAA30121.1; JOINED.
EMBL; X07096; CAA30121.1; JOINED.
EMBL; X07096; CAA30121.1; JOINED.
EMBL; X07097; CAA30121.1; JOINED.
EMBL; X07099; CAA30121.1; JOINED.
EMBL; X07099; CAA30121.1; JOINED.
EMBL; X07100; CAA30121.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-26 FROM N.A.
STRAIN=C57BL/6J;
MEDLINE=86224037; PubMed=3011788;
MEDLINE=87263407; PubMed=3603027;
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HSSP; P00480; IOTH.
SWISS-2DPAGE; P11725; MOUSE.
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354 AA;
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Best Local Similarity
Matches 35; Conserv
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TRANSIT 1
CHAIN 33
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
0rnithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
(OTCase) (Ornithine transcarbamylase).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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PROSITE; PS00097; CARBAMOYLTRANSFERASB; 1.

Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
Transit peptide. 32 MITOCHONDRION.

TRANSIT 1 32 ORNITHINE CARBAMOYLTRANSFERASE.

CHAIN
                    + L-citrulline.
PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
SUBUNIT: Homotrimer.
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BY SIMILARITY.
BY SIMILARITY.
G -> P (IN REF. 3; AAA41772).
G -> S (IN REF. 3).
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                                                                                                                  -i - SUBCELLULAR LOCATION: Mitochondrial matrix.
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Pred. No. 9.2e-21;
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Interpro; IPR002292, Orn_carbiransf.
InterPro; IPR006131, Offcace O.
InterPro; IPR006132, Offcace O.
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97.68;
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EMBL; M16933; AAA41769.1; -.
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Pfam; PF02729; OTCace N; 1.
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Shi D., Morizono H., Aoyagi M., Tuchman M., Allewell N.M.; "Crystal structure of human ornithine transcarbamylase complexed with carbamoyl phosphate and L-norvaline at 1.9 A resolution.";
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transcarbamylase gene: Structure of the 5'-end region.";
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Hata A., Fatsutki T., Shimada K., Takiguchi M., Mori M., Matsuda I.;
"Structure of the human ornithine transcarbamylase gene.";
J. Biochem. 103:302-308(1988).
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Shi D., Morizono H., Ha Y., Aoyagi M., Tuchman M., Allewell N.M.;
"1.85-A resolution crystal structure of human ornithine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Catalytic mechanism and correlation with inherited deficiency.";
J. Biol. Chem. 273:34247-34254 (1998).
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Harwinne in the leader peptide is required for both import and proteolytic cleavage of a mitochondrial precursor.";
Proc. Natl. Acad. Sci. U.S.A. 82:4930-4933(1985).
                                                                                                                                                                                                                                                                                                                                                       precursor (EC
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1 MLSNLRILLINNAALRKGHTSVVRHFWCGKPVQSQVQLKGRDL
                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-SEP-2003 (Rel. 42, Last annotation update)
Ornithine carbamoyltransferase, mitochondrial
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MEDLINE=20274073; PubMed=10813810;
                                                                                                                                                                                                                                                                                                                                                                                         (OTCase) (Ornithine transcarbamylase).
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MEDLINE=93372868; PubMed=8364586;
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Proteins 39:271-277(2000).
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                                                                                                                                                                                            STANDARD;
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REVIEW ON VARIANTS
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SEQUENCE OF 269-289 FROM N.A., AND VARIANT OTCD GLN-277.
MEDLINE=94362689; PubMed=8081373;
Gilbert-thussardier B., Rabier D., Strautnieks S., Segues B.,
Galbert-thussardier B., Rabier D., Strautnieks S., Segues B.,
Nanoreint J.-P., Munnich A.,
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carbamoyl transferase gene in two unrelated children presenting with
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MEDLINE=90269805; PubMed=2347583;
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"Use of denaturing gradient gel electrophoresis for detection of mutation and prospective diagnosis in late onset ornithine transcarbamylase deficiency."; VARIANT OTCD PRO-140.
MEDLINE=93273296; PubWed=8099056;
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MSDLINE=9273296; PubWed=8099056;
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MEDLINE=96091868; PubMed=8544185;
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InterPro; IPR001795; EF GTPbind.
InterPro; IPR004161; EFTU D2.
InterPro; IPR004161; EFTU D2.
InterPro; IPR005225; Small GTP.
InterPro; IPR00544; ITF aTF-2.
Pfam; PF00009; GTP EFTU; 1.
Pfam; PF00009; GTP EFTU; 1.
TIGRFAMS; TIGR00491; aIF-2; 1.
TIGRFAMS; TIGR00491; aIF-2; 1.
PROSITS; PRO1176; IP2; PALISE NEG.
Initiation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                  Methanosarcinales; Methanosarcinaceae; Methanosarcina
                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
FEB-2003 (Rel. 41, Last amortation update)
Probable translation initiation factor IF-2.
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                                                                     Tuchman M., Plante R.J., Giguere Y., Lemieux B.;
"The ornithine transcarbamylase gene: new 'private' mutations in four patients and study of a polymorphism.";
Hum. Mutat. 3:318-320(1994).
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                                                                                                                                                                                                                                                             "Four newly identified ornithine transcarbamylase (OTC) mutations (D126G, R129H, I172M and W332X) in Japanese male patients with earlyonset OTC deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJINE-55038770; PubMed=7951259;
Tuchman M., Plante R.J., McCann M.T., Qureshi A.A.;
"Seven new mutations in the human ornithine transcarbamylase gene.";
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MEDLINE=96400964; PubMed=8807340;
Gilbert-bussardier B., Seques B., Rozet J.-M., Rabier D., Calvas P.,
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"Partial duplication [dup. TCAC (178)] and novel point mutations
(T125M, G188R, A2209t, and H302L) of the ornithine transcarbamylase
gene in congenital hyperammonemia.";
Hum. Mutat. 8:74-76 (1996).
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MEDLINE=94362715; PubWed=8081398;
Matsuura T., Hoshide R., Kiwaki K., Komaki S., Koike B., Endo F.,
Oyanagi K., Suzuki Y., Kato I., Ishikawa K., Yoda H., Kamitani S.,
Sakaki Y., Matsuda I.;
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Guardamagna O., Gatti E., Parini R., Plante R.J., Tuchman M.;
"Genotype-phenotype correlations in ornithine transcarbamylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Garcia-Perez M.A., Sanjurjo P., Briones P., Garcia-Munoz M.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zimmer K.P., Matsuura T., Colombo J.-P., Koch H.G., Ullrich Deufel T., Harms E., Matsuda I.; "A novel point mutation at codon 269 of the ornithine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS OTCD ASN-88; CYS-176; ALA-220; TYR-302 AND LYS-343
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Pred. No. 1.7e-12;
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                                       VARIANTS OTCD LEU-117; LEU-182 AND CYS-203.
MEDLINE=94290509; PubMed=8019569;
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J. Inherit. Metab. Dis. 18:356-357(1995).
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MEDLINE=96070988; PubMed=8530002;
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Genet, 91:321-325(1993).
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2
                                                                                       Gaps
                                                                                       4
                                                            Length 597;
                                                                                      11; Indels
                                                                                                                             255 ATLDVILYDGTLKKGDTVVIGSL--GEPIQTKVRALLKPREL 294
                                                                                                                47
                                     67CAF4D902C1B8D5 CRC64;
                                                                                                                3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ--LKPRDL
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                            DB 1;
                                                              27.2%; Score 59; DB 133.3%; Pred. No. 1.4;
                                                                                                                                                                                                       591 AA
                                                                                       13; Mismatches
                                                                                                                                                                                                       PRT;
  GIP
            GTP
                                      65438 MW;
                                                                                       Conservative
                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                          IF2P METWA
ID IF2P METWA
                                                                                                                                                                               RESULT 5
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RESULT 4 IF2P_METAC

D.

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catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P00480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
ACT_SITE
ACT_SITE
                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
RR2_LOTUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
   엄
                                                                                                                                                          STRAIN-GOOL | GOL | ATCC BAA-199 | DSM 3647 | OCM 88;

STRAIN-GOOL | GOL | ATCC BAA-199 | DSM 3647 | OCM 88;

MEDLINE-2120827; PubMed-12125824,

MEDLINE-2120827; PubMed-12125824,

MARTINEZ-ARIAS R., Henne A., Wiezer A., Baeumer S., Jacobi C.,

Brueggemenier U., Johann A., Henne A., Wiezer A., Boewecke M., Steckel S.,

Brueggemenn H., Lienard T., Christmann A., Boewecke M., Steckel S.,

Bratzacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,

The genome of Methanosarcina mazei: evidence for lateral gene

The genome of Methanosarcina mazei: evidence for lateral gene

Tr rhe genome of Methanosarcina in general translation initiation by promoting

L. Mol. Microbiol. Biotechnol. 4:453-461(2002)

L. FUNCTION: Function in general translation initiation by promoting

the binding of the formylmethionine-tRNA to ribosomes. Seems to

function along with eIF-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTC_RANCA STANDARD; PRT; 350 AA.
P31326;
01-JUJ-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cornithine carbamoyltransferase, mitochondrial precursor (BC 2.1.3.3)
(OTCase) (Ornithine transcarbamylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ;
                                                                                                        Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.8%; Score 56; DB 1; Length 591; 33.3%; Pred. No. 3.7; tive 13; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAWAN, ME 00100, -1.

InterPro; IPR000795; EF GTPbind.
InterPro; IPR00178; IF GTPbind.
InterPro; IPR00178; IF2.
INTERPAMS; TIGR00491; aIF-2; I.
ITGREAMS; TIGR00491; aIR-2; I.
ITGREAMS; TIGR00491; aIR-2; I.
ITGREAMS; TIGR00491; aIR-2; I.
ITGREAMS; TIGR00491; aIR-2; I.
Interprofice factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 ATLDIILYDGTLKKGDTVVIGSL.-GEPIRTKVRALLKPREL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TP (BY SIMILARITY).

TP (BY SIMILARITY).

TP (BY SIMILARITY).

FB328265BBD887DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ--LKPRDL 42
              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable translation initiation factor IF-2.
                                                                          INFB OR MM2463.
Methanosarcina mazei (Methanosarcina frisia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 919
919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE013490; AAM32159.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          591 AA; 64900 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 33.33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
                                                                                                                                   NCBI TaxID=2209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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OTC_RANCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rep. Fac. Sci. Shizouka Univ. 29:45-54 (1995).

-!- FUNCTION: OTC IS NECESSARY FOR THE TADPOLES TRANSITION FROM AN AMMONOTELIC, AQUATIC LARVA TO A UREOTELIC, TERRESTRIAL ADULT.

-!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate + L-citrulline.

-!- FATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.

-!- SUBUNIT: HOMOCTIME.

-!- SUBCELLULAR LOCATION: Mitochondrial matrix.

-!- SUBCELLULAR LOCATION: Mitochondrial matrix.

-!- ISSUE SPECIFICITY: LIVER.

-!- DEVELOMMENTAL STAGE: EXPRESSED DURING EMBRYONIC DEVELOPMENT.

-!- INDUCTION: By thyroid hormone.

-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                         Helbing C., Gergely G., Atkinson B.G.,
"Sequential up-regulation of thyroid hormone beta receptor, ornith
transcarbamylase, and carbamyl phosphate synthetase mRNAs in the
liver of Rana catesbeiana tadpoles during spontaneous and thyroid
hormone-induced metamorphosis.";
Dev. Genet. 13:289-301(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
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PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Iwase K., Yamanchi K., Ishikawa K.;
"Molecular cloning of bullfrog (Rana catesbeiana) ornithine
transcarbamylase and induction of its mRNA during spontaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRION (BY SIMILARITY).
ORNITHING CARBAMOYLITRANSFERASE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.3%; Score 55; DB 1; Length 350; 38.1%; Pred. No. 2.9; tive 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E1E598355F03C13E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006130; Asp/orn Cotranf
InterPro; IPR002292; Orn carbtransf.
InterPro; IPR006131; OTCace_O.
InterPro; IPR006132; OTCace_P.
                                                                                                                                                                                                                       MEDLINE=93177976; PubMed=1291156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39636 MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M95193; AAA49528.1; -. EMBL; D38304; BAA22775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00185; OTCace; 1,
Pfam; PF02729; OTCace N; 1.
PRINTS; PR00100; AOTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
350
259
299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metamorphosis.";
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TRANSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 1; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
NCBI_TaxID=34305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Accession MG-20;
MEDLINE=21082929; Pubmed=11214967;
Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
"Complete structure of the chloroplast genome of a legume, Lotus
                                                                                                                                                                                                                                                                                                                       aponicus.";
NA Res. 7:323-330(2000).
-!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
0xygen-independent coproporphyrinogen III oxidase (BC 1....-)
(Coproporphyrinogensee) (Coprogen oxidase).
HERN OR STH4004 OR STY3877 OR T3617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu K., Elliott T.;
"Cloning, DNA sequence, and complementation analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.9%; Score 54; DB 1; Length 236; 38.5%; Pred. No. 2.6; ive 10; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAR, MF 0021; -; 1.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR0018018; Ribosomal_S2.
Pram; PF00318; Ribosomal_S2, 1.
PRINTS; PR00395; RIBOSOMĀLS2.
TIGRFAM; TIGR01011; rpsB bact; 1.
PROSITE; PS00962; RIBOSOMĀL_S2_1; 1.
PROSITE; PS00963; RIBOSOMĀL_S2_2; 1.
Ribosomal protein; Chloroplast.
SEQUENCE 236 AA; 26982 WW; CE9E238572325586 CRC64;
                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 30s ribosomal protein S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457 AA.
 236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 IASIRLILNKLVFAICEGHSSYIRNF 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LSNLRILLNKA--ALRKAHTSMVRNF 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=S.typhimurium; STRAIN=LT2;
MEDLINE=94252986; PubMed=8195073;
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP002983; BAB33197.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38....
Local Similarity 38....
Local Similarity 38....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=602, 601;
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                                                                                                                      japonicus.
                                                                                                                                      Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SALTY
 LOTJA
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P37129;
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HEMN_SALTY
                                                                                                                      Lotus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.typhi; STRAIN=TY2 / ATCC 700931; MEDLINE=22531367; PubMed=12644564; Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R., "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and CT18.";
J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: ANAEROBIC TRANSFORMATION OF COPROPORPHYRINOGEN-III INTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTOPORPHYRINGEN-IX.
-!- COFACTOR: REQUIRES MAGNESIUM, ATP AND NAD (OR NADP) FOR ACTIVITY.
-!- PATHWAY: POTDMYIN blosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE ANAEROBIC COPROPORPHYRINOGEN III
OXIDASE FAMILY.
                                                                                                                                                                                                                                                            McCleiland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERCIES. 179th; STRAIN=CT18;
MEDLINE=2153494; PubMed=11677608;
MEDLINE=2153494; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mingall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quall M., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence Of a multiple drug resistant Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                SPECIES-S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720,
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 26.5%; Pred. No. 5.3; 9; Conservative 10; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFÁMS; TIGR00538; hemN; 1.
Porphyrin biosynthesis; Oxidoreductase; Magnesium; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457 AA; 52828 MW; 5667B4FE76204DAB CRC64;
Salmonella typhimurium hemN gene encoding a putative oxygen-independent coproporphyrinogen III oxidase.", J. Bacteriol. 176:3196-3203(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, U06779; AAA19690.1; --
EMBL, AAL03243.1; --
EMBL, AL672260; CAD03096:
EMBL, AL67280; CAD03096:
EMBL, AE016846; AAO71118.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           StyGene; SG10154; hemN.
InterPro; IPR006638; Elp3.
InterPro; IPR004558; HemN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF04055; Radical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00729; Elp3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 457 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                            SEQUENCE FROM N.A.
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Gaps

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                                                                                                                                                                                                                                                                                                OTC PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
         Matches
                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                     SOURCE STANK NEW REPRESENTED DRIVER SOURCE STANK SOURCE SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A developmentally regulated basic-leucine zipper-like gene and its expression in embryonic retina and lens.", Proc. Natl. Acad. Sci. U.S.A. 91:1351-1355(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Chromokinesin: a DNA-binding, kinesin-like nuclear protein.";
J. Cell Biol. 128:761-768(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEUROEPITHELIUM OF EMBRYOS.
-!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
CHROMOKINESIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPINDLE STABILIZATION.
-!- SUBCELLULAR LOCATION: NUCLEAR, ASSOCIATED WITH MITOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: EXPRESSED IN PROLIFERATING CELLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KG -> RI (IN REF. 2).
MW; FA01ED83425F5875 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KINESIN-MOTOR.
COILED COIL (BY SIMILARITY)
GLOBULAR.
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
MOTOR protein; Microtubules; ATP-binding; DNA-binding;
                                                                                                                                                                                                                                                            090640; 090608;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
18-FBB-2003 (Rel. 41, Last annotation update)
Chromosome-associated kinesin KIF4A (Chromokinesin).
                                       LNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 728-1088 FROM N.A.
STRAIN=White leghorn; TISSUE=Embryonic retina;
MEDLINE=94151328; PubMed=8108415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-White leghorn; TISSUE=Embryonic retina; MEDLINE=95181533; PubMed=7876303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54; DB
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, P17119; 3KAR.
INICETPO: PFR001752; Kinesin motor.
Pfam: PF00225; Kinesin. 1.
PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U18309; AAC59666.1; -.
EMBL; U04821; AAA18960.1; -.
PIR; A56514; A56514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138923
                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1087 108
1225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang S.Z., Adler R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHROMOSOMES.
                                                                                                                                                                                                                                    CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                           KIF4A.
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                                                                                                                                                                                                                                                                      SOLUTION DE LA PRESENTATION DE LA PROPERTICIO DE LA PRESENTATION DE LA PROPERTICIO DEL PROPERTICIO DEL PROPERTICIO DE LA PROPERTICIO DEL PROPERTICIO DEL PROPERTICIO DE LA PROPERTICIO DE LA PROPERTICIO DEL PROPERTICIO D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koger J.B., Jones B.E.;
"Nucleotide sequence of porcine OTCase cDNA.";
J. Anim. Sci. 75:3368-3368(1997).
-!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Contithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
(OTCase) (Ornithine transcarbamylase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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PROSITE; PS00097; CARBAMOYLTRANSPERASE; 1.
Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 + L-citrulline.
--- PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
--- SUBUNIT: Homotrimer (By similarity).
--- SUBCELLUTAR LOCATION: Mitochondrial matrix.
--- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MITOCHONDRION (BY SIMILARITY). ORNITHINE CARBAMOYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53; DB 1; Length 328; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                     528 MSKELVELNKALALKEALAKKMIQNDSQLEPIQSOYOTNIKDL 570
2 LSNLRILLNKA-ALRKA-HTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89302B9A471CD265 CRC64;
                                                                                                                                                                                                     328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006130; Asp/Orn Cotranf. InterPro; IPR002292; Orn Carbtransf. InterPro; IPR006131; OrCace O. InterPro; IPR006132; OrCace Pfam; PF00185; OrCace, 1. Pfam; PF00182; OrCace, 1. Pfam; PF00129; OrCace N; 1. PRINTS; PR00100; AOICASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98080180; PubMed=9420013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36738 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y13045; CAA73480.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
328
237
277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transit peptide.
NON TER 1
TRANSIT <1
CHAIN 7
                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P00480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
ACT_SITE
SEQUENCE
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RESULT 11

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Gaps

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us-08-765-244-22.rsp

CGS5 YE? P30283; CGS5_YEAST

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24.4%; Score 53; DB 1; Length 435; 46.4%; Pred. No. 7; ive 4; Mismatches 11; Indels
                                          SGD; S0006324; CLBS.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:000082; P:G1/S transition of mitotic cell cycle;
GO; GO:000086; P:G2/M transition of mitotic cell cycle;
GO; GO:00006279; P:premeiotic DNA synthesis; IGI.
                                                                                                                                                                                                                                                                               SMART; SM00385, CYCLIN; 2.
PROSITE, PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Multigene family.
SEQUENCE 435 AA; 50431 MW; 5AD67EB841BA5759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SNLRILLNKAALRKAHTSMVRNFRYGKP 30
                                                                                                                                                            InterPro; IPR006670; Cyclin.
InterPro; IPR004367; Cyclin Cterm.
InterPro; IPR006671; Cyclin N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE002306; AAF39255.1; -.
  U40828; AAB68061.1; -.
                                                                                                                                                                                                                                  Pfam; PF00134; cyclin; 1. Pfam; PF02984; cyclin C; 1. SMART; SMO0385; CYCLIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; TC0398; -.
HAMAP; MF_00141; -; 1.
InterPro; IPR001059; EF-P.
                                                                                                                                                                                                                                                                                                                                                                                                                        Sest Local Similarity 46.4
Atches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                        PIR; S31290; S31290.
SGD; S0006324; CLB5.
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
FFP1 CHLMU
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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REDLINE=97313271; PubMed=9169875;

NEDLINE=97313271; PubMed=9169875;

NEDLINE=97313271; PubMed=9169875;

A araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

A raujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

A chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,

Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,

Marathe R., Messenguy F., Mewes H.-W., Mirripati S., Moestl D.,

Marathe R., Messenguy F., Mewes H.-W., Mirripati S., Moestl D.,

Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,

Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,

Achroens B., Schramm S., Schroder M., Schich A.,

Norsetarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,

Walsh S.V., Wambutt R., Wang Y., Wedler B., Wedler H., Winnett E.,

Almong W.W., Zollner A., Vo D.H., Hani J.;

Nather 187103-105 (1997).

Nather 187103-105 (1997).

Nather 187103-105 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     Epstein C.B., Cross F.R.; "CLBS: a novel B cyclin from budding yeast with a role in S phase."; Genes Dev. 6:1695-1706(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - (- FUNCTION: REQUIRED FOR BFFICIENT PROGRESSION THROUGH S PHASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED JUST BEFORE CELL CYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schwob E., Nasmyth K.; "CLBS and CLBS, a new pair of B cyclins involved in DNA replication in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSSIBLY FOR THE NORMAL PROGRESSION THROUGH MEIOSIS. INTERACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=94074543; PubMed=8253070;
McDLINE=94074543; PubMed=8253070;
Mcubme C., Linder P.;
"A new pair P.;
"A new pair B-type cyclins from Saccharomyces cerevisiae that function early in the cell cycle.";
EMBO J. 12:3437-3447(1993).
                                                                                                                                                                                                                 Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetales;
                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
3-phase entry cyclin 5.
CLBS OR YPR120C OR P9642.8.
                             435 AA.
                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                          STRAIN=BF264-15D;
MEDLINE=92387544; PubMed=1387626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93307652; PubMed=8319908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M91209; AAA34503.1; -. EMBL; X70435; CAA49893.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes Dev. 7:1160-1175(1993).
                             STANDARD;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
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                             YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
Nucleic Acids Res. 28:1397-1406(2000).
-!- FUNCTION: INVOIVED IN PEPTIDE BOND SYNTHESIS. STIMULATES EFFICIENT
-- TRANSLATION AND PEPTIDE-BOND SYNTHESIS ON NATIVE OR RECONSTITUTED
70S RIBOSOMES IN VITRO. PROBABLY PUNCTIONS INDIRECTLY BY ALTERING
THE APPLINTY OF THE RIBOSOME FOR AMINOACYL-TRNA, THUS INCREASING
THEIR REACTIVITY AS ACCEPTORS FOR PEPTIDYL TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STEATREMOPH / Nigg;
MEDLINE=20150255; PubMed=10684935;
MEDLINE=20150255; PubMed=10684935;
MEDGINE=20150255; PubMed=10684935;
Milte D., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Bisen J., Praser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia muridarum.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
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-- PATHRAY: Protein biosynthesis.
-- SUBCELLULAR LOCATION: Cytoplasmic.
-- SIMILARITY: Belongs to the elongation factor P family.
                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) ELPPI OR TC0398.
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or send an email to license@isb-sib.ch).
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SNLKILQNKRALSKNDSSSKQQVQDSKP
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SPECIES=E.col; STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
OShima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Moril H., Motcomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SPECIESE.coli, STRAIN=K12;
MEDLINE=89263708; PubMed=2657652;
Mohno T., Noji S., Taniquchi S., Saito T.;
"The narX and narL genes encoding the nitrate-sensing regulators of Escherichia coli are homologous to a family of prokaryotic two-component regulatory genes.";
Nucleic Acids Res. 17:2947-2957(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=E.coli, STRAIN=K12 / MG1655, MEDLINE=97426617; PubMed=9278503; Blactiner F.R., Plunkett G. Ill, Bloch C.A., Perna N.T., Burland V., Railey M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                        3,
                                                             Length 185;
             PROSITE; PS01275; EFP; 1.
Protein biosynthesis; Elongation factor; Complete proteome.
SEQUENCE 185 AA; 20468 MW; 969BD834F4997CE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                        Indels
                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrate/nitrite sensor protein narx (EC 2.7.3.-).
NARX OR NARR OR B1222 OR Z1998 OR ECSI727 OR SF1225.
                                                               DB 1;
                                                                                                                 42
                                                                                                                              24.2%; Score 52.5; DE
41.2%; Pred. No. 3.2;
:ive 9; Mismatches
                                                                                                               11 KAALRKAHTSMV--RNFRYGKPVOSOVOLKPRDL
                                                                                                                                                                                                      598 AA
                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                              01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                           Escherichia coli,
Escherichia coli 0157:H7, and
                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=562, 83334, 623;
                                                       Query Match
Best Local Similarity 41.29
                                                                                                                                                                                                      STANDARD;
 Pfam; PF01132; EFP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gregor J., Davis
Mau B., Shao Y.;
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P10956;
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Nature 409:529-533(2001).

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                                                       SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796; Kurokawa K., Ishii K., Yokoyama K., Hayabii T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genomes sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4432-4441 (2002).

-!- FUNCTION: ACTS AS A SENSOR FOR NITRATE/NITRITE AND TRANSDUCES SIGNAL OF NITRATE AVAILABILITY TO THE NARL PROTEIN AND OF BOTH NITRATE/NITRITE TO THE NARP PROTEIN. NARX PROBABLY ACTIVATES NARL PLAYS A NEGRITUE ROLE IN CONTROLLING NARL ACTIVITY, PROBABLY THROUGH DEPHOSPHORYLATION IN THE ABSENCE OF NITRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22272406, PubMed=12384560,
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICE OF 1-55 FROM N.A.
SPECUES=E.coli; STRAIN=K12;
MEDLINE=89318707; PubMed=2668029;
Moji S., Nohno T., Saitor T., Taniguchi S.;
"The narK gene product participates in nitrate transport induced in Escherichia coli nitrate-respiring cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-E.coli; STRAIN-K12;
MEDLINE-89197802; Pubmed-2649492;
Stewart V., Parales J. Jr., Merkel S.M.;
"Structure of genes narL and narK of the nar (nitrate reductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-60 FROM N.A. SPECIES=E.coli; STRAIN=K12 / MC4100; Cavicchioli R., Gunsalus R.P., Chiang R.C.; Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 HAMP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 171:2229-2234(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE005339; AAG56082.1; -. EMBL; AP002556; BAB35150.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           locus in Escherichia coli K-12
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EMBL; M24910; AAA24198.1; -.
EMBL; X65715; CAA46631.1; -.
EMBL; X69189; CAA48934.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEBS Lett. 252:139-143(1989)
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[5]
SEQUENCE 1
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EMBL;
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01-NOV-1997
01-NOV-1997
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DOMAIN
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REPEAT
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"Fission yeast F-box protein Pof3 is required for genome integrity and
telomere function.";
                                                                                                                                                                                                                                                                              PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
GSAHAINKAGS -> AAPMRSTKRDA (IN REF. 1 AND
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodson G., Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                          PROSITE; PS50865; HAMP; 1.
PROSITE; PS50109; HIS KIN; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation; Transmembrane; Inner membrane; Nitrate assimilation;
                                                                                                                                                                                                                                                                                                                                                 24.0%; Score 52; DB 1; Length 598; 31.0%; Pred. No. 14; ive 9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 448 LLTTFRLOLTEPGLRPALEASCEEYSAKFGFPVKLDYOLPPR 489
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886BA0FC2C8F3C3E CRC64;
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                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL) HAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                               POTENTIAL.
PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                      HISTIDINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POFB_SCHPO STANDARD; PRT; 506 AA. 009855; 0997V1; 01-FEB-1996 (Rel. 33, Created) 26-CCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                      InterPro; INTO(3594; ATPbind ATPase.)
InterPro; IPR003569; HAPP.
InterPro; IPR003661; His kina.
InterPro; IPR005467; His kina.
InterPro; IPR005467; His kina.
InterPro; IPR005467; His kina.
Pfam; PP00672; HAMP; 1.
SMART; SM00304; HAMPs C; 1.
SMART; SM00387; HATPase C; 1.
SMART; SM00388; HisKA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-box/WD-repeat protein pof11.
POF11 OR SPAC29E6.01 OR SPAC30.05.
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MEDLINE=21668955; PubMed=11809834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Biol. Cell 13:211-224(2002).
                                                                                                                                                                                                                                                                                                                          67083 MW;
                                                                                                                                                                                                                                                                                                                                                          Local Similarity 31.0 tes 13; Conservative
                                EcoGene; EG10646; narx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
NCBI TaxID=4896;
           G90844; G90844
S26137; RGECNX
                                                                                                                                                                                                                                                                                                               374
598 AA;
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POFE_SCHPO
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Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
A cliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
A Rutherford K., Rutter S., Saunders D., Seeger K., Slarp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Nocdward J., Volckert G., Aert R., Robben J., Grymonprez B.,
Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Puchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Bger P., Zimmermann W., Wedler H., Rambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
A colet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Lucas M., Rochet M., Gaillardin C., Sanchez M., Garzon A., Thode G.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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(Rel. 35, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO0678; WD REPEATS 1; 3.
PROSITE; PSSO082; WD REPEATS 2; 6.
PROSITE; PSSO294; WD REPEATS REGION; 1.
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MD 2.
MD 4.
MD 5.
MD 6.
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ProDom; PD000018; WD40; 1.
SMART; SM00326; PBOX; 1.
SMART; SM00320; WD40; 8.
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Best Local Similarity 4%...
"....s 12; Conservative
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PROSITE; PS00678; WD REPE
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Pfam; PF00400; WD40; 7.
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ID YM37_XEAST
AC Q038Z4;
DT 01-NOV-1997
DT 01-NOV-1997
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                                                                                                                                                                                                                       Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; Wiltenucleotide sequence of Saccharomyces cerevisiae chromosome XIII.",
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 81.5 kDa protein in HLJ1-SMP2 intergenic region.
YMR163C OR YM8520.12C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.5%; Score 51; DB 1; Length 705; 36.8%; Pred. No. 23; tive 5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S54521; S54521.
SGD; S0004773; YMR163C.
Hypothetical protein.
SEQUENCE 705 AA; 81466 MW; E4F2A4D205A98F66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z49705; CAA89799.1; -.
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Best Local Similarity 36.88
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                Nature 387:90-93(1997).
                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
PubMed=9169872;
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Search completed: December 3, 2003, 14:32:56 Job time : 12 secs

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0; Gaps

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RESULT 1
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Q&r188 mus musculu
Q&r10 bos taurus
Q&3786 rattus norv
Q@iau8 trachemys s
Q@iau8 trachemys s
Q@iau8 trachemys s
Q@iau8 trachemys s
Q@iau8 trachems s
Q@iau9 arabidopsis
Q@iau9 arabidopsis
Q@im3 arabidopsis
Q@im3 arabidopsis
Q@im3 arabidopsis
Q@im3 arabidopsis
Q@avs9 xenopus lae
Q@f570 drcsophila
Q@gpg3 drcsophila
Q@gpg3 drcsophila
                                                                               December 3, 2003, 14:29:02; Search time 34 Seconds (without alignments) 326.361 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                   1 MLSNLRILLINKAALRKAHTS..........NFRYGKPVQSQVQLKPRDLC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                    830525
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                       830525 seqs, 258052604 residues
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                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
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08R1A8

09N1A7

063786

091AV8

023351

097W55

097W5

097W55

097W59

097W59

097W59

097W39

097W39

097W39

097W39

096570
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sp_virus:*
sp_vortebrate:*
sp_unclassified:*
sp_rvirus:*
sp_roteriap:*
sp_archeap:*
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                              SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_fungi:*
5: sp_invertebrate:*
6: sp_mammal:*
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sp_organelle:*
sp_phage:*
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217
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Match Length DB
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Perfect score:
                                                                                                                                                                                               Scoring table:
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ALIGNMENTS

P70518	1518 19761 Page 1970 .	Egg	, ,	6
A P		1 141		
H	1997 (TrEMBLrel. 02,	Created)		
DŢ	(TrEMBLrel. 02,	Last sequ	ence	sequence update)
DT	3 (TrEMBLrel. 23,		tatio	Last annotation update)
DE	Ornithine carbamoyltransferase		BOL	precursor (Fragment).
SO	Rattus norvegicus (Rat).			
ပ္ပ	Eukaryota; Metazoa; Chordata;		a; Ve	Craniata; Vertebrata; Euteleostomi;
ပ္ပ	Mammalia; Eutheria; Rodentia;	Sciuros	mathi	Sciurognathi; Muridae; Murinae; Rattus.
N X	NCBI_TaxID=10116; [1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85051832; PubMed=6548714;	714;		
R.	McIntyre P., Graf L., Mercer	J., Pete	rson	L., Mercer J., Peterson G., Hudson P.J.,
RA	Hoogenraad N.;			
RI	"A highly basic N-terminal extension of the mitochondrial matrix	tension	of th	ne mitochondrial matrix
RI	enzyme ornithine transcarbamylase from rat liver.";	lase fro	m rat	: liver.";
RL	FEBS Lett. 177:41-46(1984).			
DR				
DR	HSSP; P00480; 10TH.			
DR	IPR006130; Asp/Orn_	COtranf.		
DR	InterPro; IPR006132; OTCace_P			
DR	Pfam; PF02729; OTCace N; 1.			
DR	PROSITE;	ANSFERAS	д; Д;	
Š	Signal; Transferase.			
FI	SIGNAL 1	POTENTIAL.		
FI	CHAIN 33 >	ORNITHINE		CARBAMOYLTRANSFERASE.
FI	NON TER 102 1			
ÖS.	SEQUENCE 102 AA; 11932 MW;		1F19E	B739D41F19BF720D CRC64;
ŏ	h 91.7%;	Score 199; DB 11;	1 , 6	B_11; Length 102;
ăğ	Best Local Similarity 97.6%; Matches 41: Conservative 0	Pred. No. 9e-0	tches	9e-22; hes 1; Indels 0; Gaps
δ	1 MLSNLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL	MVRNFRYC	KPVQ	SQVQLKPRDL 42
Dp	1 MLSNLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQLKGRDL	MVRNFRYC	KPVQ	SOVOLKGRDL 42

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Gaps

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Indels

RESULT 2

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MEDLINE=86106223; PubMed=3943133;
Horwich A.L., Kalousek F., Fenton W.A., Pollock R.A., Rosenberg L.E.;
"Targeting of pre-ornithine transcarbamylase to mitochondria:
definition of critical regions and residues in the leader peptide.";
Cell 44:451-459(1986).
EMBL; M12583; AAA41770.1; -.
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimogiri T., Koyanagi K., Mannen H., Tsuji S.;
"Ornithine transcarbamylase is expressed in uricotelic animals.";
submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF134846; AAF61410.1;
HSSP; P00480; 10TH.
InterPro; IPR002130; Asp/orn_Cotranf.
InterPro; IPR006131; OrCace O.
InterPro; IPR006131; OrCace O.
InterPro; IPR006131; OrCace O.
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Nakaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
NCBL_TaxID=31138;
                                                                                  1 MLFHLRTLINNAALRNGHNFVVRNFRCGQPLQDKVQLKGRDL 42
                                                         1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
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Last annotation update)
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Last annotation update)
                    10;
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  Pred. No. 7.1e-11;
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                    5; Mismatches
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64.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-MRR-2003 (TrEMBLrel. 23, Ornithine transcarbamylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00185; OTCace; 1.
Pfam; PF02729; OTCace N; 1.
PRINTS; PR00100; AOTCASE.
                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 66.7
Matches 24; Conservative
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                      27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9IAU8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9IAU8
                                                                                                                                                                                              983786
                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
Q9IAU8
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Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae, Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimogiri T., Koyanagi K., Mannen H., Tsuji S.; "Ornithine transcarbamylase is expressed in uricotelic animals."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF134841; AAF61405.1; -. HSSP; P00480; 10TH.
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.6%; Score 164; DB 11; Length 351; 83.3%; Pred. No. 5.9e-16; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 354;
                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (MPR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interer,
Interpro; IPROUGLE,
Interpro; IPROUGLE,
Pfam, PF02729; OTCace, 1.
Pfam, PF02729; OTCace, N. 1.
TIGREAMS; TIGROGES, Orni, carb, tr; 1.
TIGREAMS; TIGROGES,
ORNI, EBB38BB2FC779F42 CRC64;
OFCARAGE, AA, 39365 MW, E6B38BB2FC779F42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0100; AOTCASE,
TIGRPAMS; TIGR00658; orni carb tr; 1.
PROSITE; PS00097; CARBAMOVITRANSFERASE; 1.
SEQUENCE 354 AA; 39842 MW; 30EACZEF4AC1D71B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLSNLRILLINNAALRKGHTSVVRHFWCGKPVQSQVQLKGRDL 42
                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                351 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 130;
                                                                                                QBRIA8;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seque
01-JU-ARA-2003 (TrEMBLrel. 23, Last annot
Similar to ornithine transcarbamylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006130; Asp/orn Cotranf.
InterPro; IPR002292; orn carbtransf.
InterPro; IPR006131; OTCace O.
InterPro; IPR006132; OTCace P.
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006130; Asp/Orn Cotranf.
InterPro; IPR002292; Orn_carbtransf.
InterPro; IPR006131; OTGace_O.
InterPro; IPR006132; OTCace_P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC024893; AAH24893.1; -.
HSSP; P00479; 3CSU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.98;
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Pfam; PF02729; OTCace N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9N1U7;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
Ornithine transcarbamylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 83.3
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                PRELIMINARY;
                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
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RESULT 3 Q9N1U7

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Gaps

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Length 354;
TIGRRAMS; TIGRO0658; orni carb tr; 1.
PROSITE; PS00097; CARBANOTLTRANSFERASE; 1.
SEQUENCE 354 AA; 39958 WW; BD6A2C3AEC0F99BE CRC64;
                                                                                 Score 106; DB 13;
Pred. No. 2.7e-07;
                                                                                 48.8%;
                                                                                   Query Match
Best Local Similarity
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Gaps

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ABBLINE=21332296; PubMede=11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Char-Weinher C.C.-Y., Clausen I.G., Curtis B.A.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder F., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
The complete ganome of the crenarchaeon Sulfolobus solfataricus P2.",
Proc. Natl. Acad. Sci. U.S.A., 98:7835-7840(2001).
          Obermaier B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ILLNKAA-----LRKAHTSMVRNFRY----GKPVQSQVQ-----LKPRDL 42
Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Oberma. Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T., Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C., Delseny M., Voek M., Volckaert G., Mewes H.W., Klosterman S., Schueller C., Chalwatzis N.;
"Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 61; DB 10; Length 1286;
Pred. No. 5.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.6%; Score 60; DB 17; Length 351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; Z97337; CAB10276.1; -.
EMBL; Al161540; CAB1039.1; -.
Hypothetical protein.
SEQUENCE 1286 AA; 143860 MW; F953B283C53D0DEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPRO04095; TGS_dom.
Pfam: PRO8824; TGS; 1.—
Hypothetical protein; Complete proteome.
SEQUENCE 351 AA; 39916 MW; 046A96BF004865DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vi-vui-zuul (TrEMBLrel, 18, Last sequence update) 01-JUN-2002 (TrEMBLrel, 21, Last annotation update) Hypothetical GTP binding protein SS02385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 SNLRRMLSSSSTTKRDESLVRNLLLVSPIQLDIQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 35092 / DSM 1617 / P2;
                                                                                                                                                                                                                                                                                                                                                                                                                            Match 28.1%;
Local Similarity 38.2%;
We 13; Conservative
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01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.68;
                                                                                                                                                                                   Nature 391:485-488(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q9YHY9
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MEDLINE=98121113; PubMed=9461215;
Bevan M., Bant E., Love K., Goodman H., Dean C.,
Beryamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,
Wedler E., Wambutt R., Weitzenegger T., Pohl T.M., Terryn N.,
Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,
Entian K.D., Rieger M., Schaeffer M., Punk B., Mueller-Auer S.,
Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Lepidosauria, Squamata, Iguania, Iguanidae, Phrynosomatinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimogiri T., Koyanagi K., Mannen H., Tsuji S.;
"Ornithine transcarbamylase is expressed in uricotelic animals.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Indels
                                                     1 MLSNLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                    1 MLFNLRNLLNAATLRNSSKQLVQHFRSGQPTQTNINLKGRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01D49CCB93E4DBD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLSNLRILLNKAALRKAHTSMVRNFRY--GKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                       Sceloporus undulatus (Eastern fence lizard) (Skink).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                Last annotation update)
                                                                                                                                                                                                                                                                                                   sequence update)
                                                                                                                                                                                                                                 356 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1286 AA
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PROOLOO; ACTCĀSĒ.
TIGRRAMS; TIGROGES; CTNI CALD LT; 1.
PROSITE: SOUGO?; CREBAMOVLITRĀNSFERASĒ; 1.
SEQUENCE 356 AA; 40399 MW; 01D49CCB93E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cress).
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InterPro; IPR002292; Orn_Carbtransf.
InterPro; IPR006131; OTCace_O.
InterPro; IPR006132; OTCace_P.
                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                      Last
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       7;
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                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00185; OTCace; 1.
Pfam; PF02729; OTCace_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF134844; AAF61408.1;
                                                                                                                                                                                                                                                                                                                                                       Ornithine transcarbamylase.
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       Conservative
                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P00480; 10TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8520;
          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sceloporus.
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       Matches
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Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                      NCBI_TaxID=3702;
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01-OCT-2000
                                                                                                                                    01-OCT-2000
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                           Q9LMN3;
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                                                                                                                 Q9LMN3
                                                                                               RESULT 11
Q9LMN3
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044679
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                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morona J.K., Morona R., Paton J.C.,
"Comparative genetics of capsular polysaccharide biosynthesis in
Streptococcus pneumoniae types belonging to serogroup 19.";
J. Bacteriol. 181:555-5364 (1999).
EMBL; AF105116; AAD19925.1;
InterPro; IRR001296; Glyco_trans 1.
Plan; PP00534; Glycos_trans 1.
Plan; PP00534; Glycos_trans 1.
                                                                                                                                                                                                                                                                                                                                                                                             ·.
                                                                                                                                                                                                                                                                                                                                                                       26.3%; Score 57; DB 13; Length 354; 40.5%; Pred. No. 5.5; ive 4; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                                                                                                                                                      40245 MW; 20447180BAD9D4ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43229 MW; FCFCFD5C106AC8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
           Ornithine transcarbamylase precursor (EC 2.1.3.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 AA
                                                                                                                                                                                                                                                                                                                          TIGRFAME; TIGRO0658; orni_carb_tr; 1.
PROSITE; PS00097; CARBAMOYLITRANSFERASE; 1.
                                                                                                                                                                                                                                             HASS; P00480; 10TH.
InterPro; IPR006130; Asp/Orn_Cotranf.
InterPro; IPR002292; Orn_carbtransf.
InterPro; IPR006131; OrGace_O.
InterPro; IPR006132; OrCace_O.
                                                                                                                                                                              AF065630; AAD33083.1; JOINED.
AF065631; AAD33083.1; JOINED.
AF065632; AAD33083.1; JOINED.
AF065634; AAD33083.1; JOINED.
AF065635; AAD33083.1; JOINED.
AF065636; AAD33083.1; JOINED.
AF065636; AAD33083.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative glucosyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 40.5%;
les 17; Conservative
                                                                                                                                                                        AF065638; AAD33083.1;
                                                                                                                                                                                                                                                                                                        OTCace N; 1.
                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0100; ACTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                             Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                              Pfam; PF00185; Orcace;
                                                                                                                                                                                                                                                                                                                                                      354 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                  NCBI TaxID=9031;
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EMBL;
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EMBL;
EMBL;
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Matches
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=cv. Columbia;
Liu S.X., Sakano H., Yu G., Etgu P., Lee J.M., Lenz C., Pham P.,
Liu S.X., Sakano H., Chin C., Choi E., Chung M.,
Toriumi M., Byun E., Chan A., Chin C., Choi E., Chung M.,
Goldsmith A., Gonzalez A., Liu A., Smith A., Vaysberg M., Altafi H.,
Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.F.,
Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M.,
Federspiel N.A., Theologis A.;
The sequence of BAC Fleft from Arabidopsis thaliana chromosome 1.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AASR31641, AAFR315411. -
SEQUENCE 454 AA, 50928 MW; 70BCZACCG9DEBDCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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NCBI_TaxID=6239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosid
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 454;
     Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                   Indels
                                                                                                   43
                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                             48 NVHKVLVRLGIKKSDMSMT----YIKYAENOVHLSPEDVC
                                                14;
                                                                                                   4 NLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
     DB 2;
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25.8%; Score 56; DB 2
32.5%; Pred. No. 8.1;
iive 9; Mismatches
                                                                                                                                                                                                                                                                            454 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 KAALRKAHT-SMVRNFRYGKPVQSQVQLKPR 40
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STRAIN=Bristol N2;
David M., Wohldmann P., Bauer C., Antoniou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.6%; Score 55.5; 45.2%; Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                          F16F4.13 protein.
F16F4.13.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                       PRT;
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 15,
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                                                13; Conservative
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SEQUENCE 866
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JON-2001 (TrEMBLrel. 17, Last annotation update)
01-JON-2001 (TrEMBLrel. 17, Last annotation update)
01-JON-2001 (TrEMBLrel. 17, Last annotation update)
CG10561 OR ANON-37CS OR CS.
Drosophila lebanonensis (Fruit fly) (Scaptodrosophila lebanonensis)
Bukaryota, Arthropoda, Haxapoda, Insecta, Pterygota,
Meoptera, Endoperrygota, Diptera, Brachycera, Muscomorpha,
Bphydroidea, Drosophilidae, Scaptodrosophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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MEDLINE=99250256; PubMed=10231575;
Tatarenkov A., Saez A.G., Ayala F.J.;
"A compact gene cluster in drosophila: the unrelated Cs gene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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24.9%; Score 54; DB 13; Length 457;
Best Local Similarity 46.4%; Pred. No. 20;
Matches 13; Conservative 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 300;
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041284, AAH1284.1; -.
Hypothetical protein:
SEQUENCE 457 AA; 51021 MW; EE44FE225DD0039B CRC64;
                                                                                                                                                                                                          "Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, FR030051, ARB94269.1;
WormPep; C14C6.13, CE08168.
Hypotherical procein.
SEQUENCE 300 AA; 33753 MW; 227DF298FFD8AC83 CRC64;
"The sequence of C. elegans cosmid C14C6.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to hypothetical protein MGC11993.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 24.9%; Score 54; DB 5; Best Local Similarity 31.4%; Pred. No. 13; Matches 11; Conservative 10; Mismatches 1
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                                                                                                                                              STRAIN=Bristol N2;
Waterston R.;
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                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         096570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8AVS9
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096570
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Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 24.9%; Score 54; DB 5; Length 544; Best Local Similarity 34.2%; Pred. No. 25; Matches 13; Conservative 5; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.9%; Score 54; DB 5; Length 866; 33.3%; Pred. No. 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schulz C., Perezgasga L., Fuller M.T.,
"Functional analysis of a Drosophila puromycin-sensitive aminopeptidase gene.",
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF327435, AAC48733.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
Gene 231:111-120(1999).
-!- FUNCTION: HAS A NONVITAL FUNCTION (BY SIMILARITY).
-!- SUBCELLUIAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
EMBL; AF091239; AAC67584.1; -.
FlyBase; FEGN0025668; Dleb\CG10561.
InterPro; IPR002937; Amino oxidase.
InterPro; IPR002937; Amino oxidase.
InterPro; IPR002937; Amino oxidase.
France FOR STAND OXID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 VLKNFSAILFKPALPLEKLQAIRNLGYGNÞVKIYLAYK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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InterPro; IPR001930; Ala peptase.
InterPro; IPR001914; HPr_SerP_site.
InterPro; IPR006025, Zn WTpeptdse.
Pfam; PF0143; Peptidase M1; IPR06175; PR00756; ALADIPTESE.
PROSITE; PR00756; ALADIPTESE.
PROSITE; PS00142; ZINC_PROTEASE; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
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